

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 30, 2005, 22:02:03 ; Search time 160 Seconds  
(without alignments)  
16.921 Million cell updates/sec

Title: US-09-874-350C-210

Perfect score: 40

Sequence: 1 YHDAVP 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseq1980s:\*

2: Geneseq1990s:\*

3: Geneseq2000s:\*

4: Geneseq2001s:\*

5: Geneseq2002s:\*

6: Geneseq2003as:\*

7: Geneseq2003bs:\*

8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	7	4	AAG73298
2	40	100.0	7	5	ABU60447
3	40	100.0	7	5	ABU60385
4	40	100.0	7	8	ADN88521
5	40	100.0	7	8	ADN88514
6	40	100.0	7	8	ADN88520
7	40	100.0	8	2	AAR34855
8	40	100.0	10	1	AAP80605
9	40	100.0	10	2	AAR34851
10	40	100.0	10	2	AAW31092
11	40	100.0	10	4	AAB32087
12	40	100.0	10	4	AAG34006
13	40	100.0	10	8	ADN88517
14	40	100.0	14	2	AAW29953
15	40	100.0	14	4	AAG73121
16	40	100.0	14	4	AAG73120
17	40	100.0	14	4	AAG73119
18	40	100.0	14	5	AAW50413
19	40	100.0	14	8	ADN88359
20	40	100.0	14	8	ADN88361
21	40	100.0	14	8	ADN88360
22	40	100.0	14	8	ADN88522
23	40	100.0	15	8	ADN88517
24	40	100.0	16	4	AAG73124
25	40	100.0	16	4	AAG73123

26	40	100.0	16	4	AAG73122	Aag73122	Protease
27	40	100.0	16	8	ADN88518	Adn88518	Fluorogen
28	40	100.0	16	8	ADN88362	Adn88362	Fluorogen
29	40	100.0	16	8	ADN88523	Adn88523	Fluorogen
30	40	100.0	16	8	ADN88363	Adn88363	Fluorogen
31	40	100.0	16	8	ADN88364	Adn88364	Fluorogen
32	40	100.0	17	2	AAR21431	Aar21431	Biotinyl
33	40	100.0	17	4	AAG73125	Aag73125	Protease
34	40	100.0	17	7	ABU64171	Abu64171	Caspase p
35	40	100.0	17	8	ADN88365	Adn88365	Fluorogen
36	40	100.0	17	8	ADN88366	Adn88366	Fluorogen
37	40	100.0	17	8	ADN88368	Adn88368	Fluorogen
38	40	100.0	17	8	ADN88367	Adn88367	Fluorogen
39	40	100.0	17	8	ADN88369	Adn88369	Fluorogen
40	40	100.0	18	4	AAG73237	Aag73237	Protease
41	40	100.0	18	4	AAG73129	Aag73129	Protease
42	40	100.0	18	4	AAG73235	Aag73235	Protease
43	40	100.0	18	4	AAG73126	Aag73126	Protease
44	40	100.0	18	4	AAG73236	Aag73236	Protease
45	40	100.0	18	4	AAG73128	Aag73128	Protease
46	40	100.0	18	4	AAG73127	Aag73127	Protease
47	40	100.0	18	4	AAG73130	Aag73130	Protease
48	40	100.0	18	8	ADN88370	Adn88370	Fluorogen
49	40	100.0	18	8	ADN88474	Adn88474	Fluorogen
50	40	100.0	18	8	ADN88524	Adn88524	Fluorogen
51	40	100.0	18	8	ADN88475	Adn88475	Fluorogen
52	40	100.0	18	8	ADN88516	Adn88516	Fluorogen
53	40	100.0	18	8	ADN88525	Adn88525	Fluorogen
54	40	100.0	19	1	AAP61520	Aap61520	Sequence
55	40	100.0	199	1	AAP61521	Aap61521	Sequence
56	40	100.0	202	2	AAP52020	Aap52020	Truncated
57	40	100.0	238	1	AAP60307	Aap60307	Sequence
58	40	100.0	238	1	AAP70306	Aap70306	Sequence
59	40	100.0	238	2	AAR42447	Aar42447	Human int
60	40	100.0	269	1	AAP50043	Aap50043	Sequence
61	40	100.0	269	1	AAP81197	Aap81197	Interleuk
62	40	100.0	269	2	AAR15747	Aar15747	Interleuk
63	40	100.0	269	2	AAR42213	Aar42213	Human int
64	40	100.0	269	2	AAW31668	Aaw31668	Precursor
65	40	100.0	269	2	AAW71382	Aaw71382	Interleuk
66	40	100.0	269	2	AAW08322	Aaw08322	Human IL-
67	40	100.0	269	3	AAW69531	Aay69531	Human int
68	40	100.0	269	3	AAB37790	Aab37790	Human int
69	40	100.0	269	4	AAB35251	Aab35251	Human pre
70	40	100.0	269	4	AAB37079	Aab37079	Human IL1
71	40	100.0	269	5	AAU80166	Aau80166	Human int
72	40	100.0	269	5	AAU11115	Aau11115	Human int
73	40	100.0	269	5	AAE33364	Aae33364	Human int
74	40	100.0	269	6	ABU08119	Abu08119	Recombina
75	40	100.0	269	6	ABO10812	Abol0812	Human int
76	40	100.0	269	7	ADC78855	Adc78855	Human PRO
77	40	100.0	269	7	ADD18660	Adh18660	Human dis
78	40	100.0	269	8	ADH17054	Adh17054	Human int
79	40	100.0	269	8	ADN07707	Adn07707	Human bet
80	40	100.0	269	8	ABM80337	Abm80337	Tumour-as
81	40	100.0	269	8	ADP54072	Adp54072	Human PRO
82	40	100.0	295	1	AAP60326	Aap60326	Interleuk
83	40	100.0	295	1	AAP60680	Aap60680	Prepro- a
84	40	100.0	295	2	AAR14855	Aar14855	Mature In
85	40	100.0	295	2	AAI33271	Aay33271	Interleuk
86	36	90.0	538	2	AAR34852	Aar34852	IL-1beta
87	36	90.0	10	2	AAR34852	Aar34852	IL-1beta
88	36	90.0	14	4	AAG73329	Aag73329	Protease
89	36	90.0	14	4	AAU10757	Aau10757	Target pe
90	36	90.0	14	4	AAU10760	Aau10760	LEPB subs
91	36	90.0	268	2	AAR06358	Aar06358	Monkey IL
92	33	82.5	16	8	ADN88476	Adn88476	Fluorogen
93	33	82.5	83	4	AAW88306	Aaw88306	Human imm
94	33	82.5	272	7	ADB70030	Adb70030	C. neofor
95	33	82.5	419	5	AAU72965	Aau72965	Weisseria
96	33	82.5	419	5	AAU72938	Aau72938	Weisseria
97	33	82.5	451	4	ABG24306	Abg24306	Novos hum
98	33	82.5	1172	4	ABB72034	Abb72034	Drosophil

99 32 80.0 10 2 AAR34854  
100 32 80.0 179 3 AAB43346  
101 32 80.0 213 6 ABU43165  
102 32 80.0 223 5 ABP39353  
103 32 80.0 223 8 AD804519  
104 32 80.0 295 4 AAB96522  
105 32 80.0 306 5 ABM47371  
106 32 80.0 361 7 ADM25885  
107 32 80.0 422 7 ADH87758  
108 32 80.0 914 5 AAG66094  
109 31 77.5 60 6 ABP97620  
110 31 77.5 60 6 ABP97622  
111 31 77.5 241 4 AAG25707  
112 31 77.5 259 6 ABU25558  
113 31 77.5 313 4 ABG14394  
114 31 77.5 359 5 ABP66050  
115 31 77.5 481 7 ADF08036  
116 31 77.5 691 4 AAG81212  
117 31 77.5 691 6 ABU36904  
118 31 77.5 691 6 ABU34715  
119 31 77.5 694 6 ABU35998  
120 31 77.5 849 4 ABP59837  
121 31 77.5 1090 7 AB074403  
122 30 75.0 7 5 AAM50414  
123 30 75.0 7 6 ABP57519  
124 30 75.0 7 8 ADJ84027  
125 30 75.0 7 8 ADP74560  
126 30 75.0 8 6 ABP57513  
127 30 75.0 8 6 ABRA40075  
128 30 75.0 9 1 AAP80612  
129 30 75.0 19 1 AAP80607  
130 30 75.0 52 5 ABP07136  
131 30 75.0 60 6 ABP97609  
132 30 75.0 101 6 ABUS0204  
133 30 75.0 105 6 ABU23090  
134 30 75.0 183 4 AAU19866  
135 30 75.0 183 5 ABP48086  
136 30 75.0 183 7 ADC11048  
137 30 75.0 197 2 AAW28345  
138 30 75.0 220 6 ABU45680  
139 30 75.0 221 4 ABM67690  
140 30 75.0 237 3 AAG33217  
141 30 75.0 243 7 ADM26993  
142 30 75.0 249 6 ABM67423  
143 30 75.0 251 3 AAG33216  
144 30 75.0 251 5 ABU05705  
145 30 75.0 251 2 ABU05672  
146 30 75.0 275 2 AAU36134  
147 30 75.0 310 6 ABU18308  
148 30 75.0 335 4 ABM58955  
149 30 75.0 336 6 ABU16120  
150 30 75.0 336 6 ABM72635

## ALIGNMENTS

RESULT 1  
AAG73298  
ID AAG73298 standard; peptide; 7 AA.

AC AAG73298;

XX 14-AUG-2001 (first entry)

XX Protease indicator compound peptide #27.

XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
KW haemophilia.

XX Synthetic.

AAR34854 IL-lbета  
AAB43346 Human ORF  
ABU43165 Protein e  
ABP39353 Staphyloc  
AD804519 Staphyloc  
AAB96522 Putative  
ABM47371 Listeria  
ADM25885 Hyperther  
ADH87758 Interococ  
AAG66094 Soybean a  
ABP97620 Amino aci  
ABP97622 Amino aci  
ABG25707 Novel hum  
ABU25558 Protein e  
ABG14394 Novel hum  
ABP66050 Bifidobac  
ADF08036 Bacterial  
AAG81212 Mycobacte  
ABU36904 Protein e  
ABU34715 Protein e  
ABU35998 Protein e  
ABP59837 Drosophil  
ABO74403 Pseudomon  
AAM50414 Tumour as  
ABP57519 Different  
ADJ84027 Apoptosis  
ADP74560 Caspase-1  
ABP57513 Different  
ABR40075 Dendrimer  
AAP80612 Sequence  
AAP80607 Sequence  
ABP07136 Human ORF  
ABP97609 Amino aci  
ABUS0204 Protein e  
ABU23090 Protein e  
AAU19866 Human nov  
ABP48086 Human pol  
ADC11048 Human pro  
AAW28345 Staphyloc  
ABU45680 Protein e  
ABM67690 Drosophil  
AAG33217 Zea mays  
ADM26993 Hyperther  
ABM67423 Phototrab  
AAG33216 Zea mays  
ABU05705 M. tuberc  
ABU05672 M. tuberc  
AAU36134 Streptom  
ABU18308 Protein e  
ABM58955 Drosophil  
ABU16120 Protein e  
ABM72635 Staphyloc

PN WO200118238-A1.  
XX  
PD 15-MAR-2001.  
XX  
XX 11-SEP-2000; 2000WO-US024882.  
PF  
XX  
XX AAB96522 Putative  
PR 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
PA  
XX Komoriya A, Packard BS;  
PI  
XX WPI; 2001-389573/41.  
DR  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
XX Claim 1; Page 70; 86pp; English.  
PS  
XX The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 40; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YVHDAPV 7  
Db 1 YVHDAPV 7  
|||||  
|||  
  
RESULT 2  
ABU60447  
ID ABU60447 standard; peptide; 7 AA.  
AC ABU60447;  
XX  
XX 29-APR-2003 (first entry)  
DT  
XX  
XX Protease binding peptide motif SEQ ID 171.  
DE  
XX  
KW Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;  
KW nuclease; screening; fluorophore; substrate cleavage.  
XX  
XX Synthetic.  
XX  
XX WO200261038-A2.  
PN  
XX  
XX 08-AUG-2002.  
PD  
XX  
XX 21-DEC-2001; 2001WO-US049781.  
PF  
XX  
XX 22-DEC-2000; 2000US-00747287.  
PR  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
PA  
XX Packard BS, Komoriya A;  
PI  
XX WPI; 2002-698548/75.  
DR  
XX  
XX Indicator composition comprising polypeptide or nucleic acid backbone  
PT joining two same chromophores resulting in quenching of fluorescence  
PT of/change in absorbance of chromophores, useful for detecting protease

PT activity.

PS Disclosure; Page 35; 97pp; English.

XX This invention describes a novel indicator composition (referred as homo-

XX doubly labeled compositions) comprising a polypeptide backbone or a

XX nucleic acid backbone joining two chromophores of the same species

XX whereby the chromophores form an H-dimer resulting in quenching of the

XX fluorescence of or a change in the absorbance of the chromophore, a

XX decrease in fluorescence or a change in absorbance indicates that the

XX first molecule and the second molecule are interacting. The indicator is

XX useful for detecting the activity of a protease, where an increase in

XX fluorescence or a change in absorbance indicates that the protease

XX cleaves the polypeptide backbone. The indicator is attached to a solid

XX support inside a mammalian, yeast or insect cell. The composition bears a

XX hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-

XX fluorinecarboxylic group, 9-fluoreneacetyl group, and 9-fluorenone-1-

XX carboxylic group, benzyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-

XX methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-

XX benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-

XX dimethoxybenzhydryl (Mbh), etc. The method described in the invention is

XX useful for detecting protease or nuclease activity (or the presence of

XX nucleic acid) in histological section, cells in culture (e.g., seeded or

XX cultured adherent cells), a biological sample such as tissue, biopsy,

XX lymph, embryo, or whole animal, or cell suspension derived from a

XX biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.

XX The indicator composition is also useful for screening a test agent for

XX the ability to modulate a protease (or a nuclease, lipase, etc.). The

XX indicator reagents allow rapid determination of protease activity in a

XX matter of minutes in a single-step procedure. The fluorescent indicators

XX both absorb and emit in the visible range (400-800 nm). These signals are

XX therefore not readily quenched by, nor is activation of the fluorophores,

XX that is, absorption of light, interfered with by background molecules;

XX therefore they are easily detected in biological samples. The fluorogenic

XX protease indicators utilise high efficiency fluorophores and are able to

XX achieve a high degree of quenching while providing a strong signal when

XX the quench is released by cleavage of the peptide substrate. The high

XX signal allows detection of very low levels of protease activity. Thus the

XX fluorogenic protease indicators are particularly well suited for in situ

XX detection of protease activity. ABU60357-ABU60477 represent peptides use

XX to illustrate the method described in the disclosure of the invention

SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7

Db 1 YVHDAPV 7

RESULT 3

ID ABU60385

AC ABU60385 standard; peptide; 7 AA.

XX 29-APR-2003 (first entry)

XX Protease binding peptide motif SEQ ID 55.

XX Protease; indicator; chromophore; H-dimer; fluorescence; absorbance;

XX nuclease; screening; fluorophore; substrate cleavage.

XX Synthetic.

XX WO200261038-A2.

XX 08-AUG-2002.

XX 21-DEC-2001; 2001WO-US049781.

XX 22-DEC-2000; 2000US-00747287.

XX (ONCO-) ONCOIMMUNIN INC.

XX Packard BS, Komoriya A;

XX WPI; 2002-698548/75.

XX Indicator composition comprising polypeptide or nucleic acid backbone

XX joining two same chromophores resulting in quenching of fluorescence

XX of/change in absorbance of chromophores, useful for detecting protease

XX activity.

XX Disclosure; Page 31; 97pp; English.

XX This invention describes a novel indicator composition (referred as homo-

XX doubly labeled compositions) comprising a polypeptide backbone or a

XX nucleic acid backbone joining two chromophores of the same species

XX whereby the chromophores form an H-dimer resulting in quenching of the

XX fluorescence of or a change in the absorbance of the chromophore, a

XX decrease in fluorescence or a change in absorbance indicates that the

XX first molecule and the second molecule are interacting. The indicator is

XX useful for detecting the activity of a protease, where an increase in

XX fluorescence or a change in absorbance indicates that the protease

XX cleaves the polypeptide backbone. The indicator is attached to a solid

XX support inside a mammalian, yeast or insect cell. The composition bears a

XX hydrophobic group such as Fmoc, 9-fluoreneacetyl group, 1-

XX fluorinecarboxylic group, 9-fluoreneacetyl group, and 9-fluorenone-1-

XX carboxylic group, benzyloxycarbonyl, Xanthyl (Xan), Trityl (Trt), 4-

XX methyltrityl (Mtt), 4-methoxytrityl (Mmt), 4-methoxy-2,3, 6-trimethyl-

XX benzenesulphonyl (Mtr), Mesitylene-2-sulphonyl (Mts), 4,4'-

XX dimethoxybenzhydryl (Mbh), etc. The method described in the invention is

XX useful for detecting protease or nuclease activity (or the presence of

XX nucleic acid) in histological section, cells in culture (e.g., seeded or

XX cultured adherent cells), a biological sample such as tissue, biopsy,

XX lymph, embryo, or whole animal, or cell suspension derived from a

XX biological sample such as tissue, blood, urine, saliva, lymph, or biopsy.

XX The indicator composition is also useful for screening a test agent for

XX the ability to modulate a protease (or a nuclease, lipase, etc.). The

XX indicator reagents allow rapid determination of protease activity in a

XX matter of minutes in a single-step procedure. The fluorescent indicators

XX both absorb and emit in the visible range (400-800 nm). These signals are

XX therefore not readily quenched by, nor is activation of the fluorophores,

XX that is, absorption of light, interfered with by background molecules;

XX therefore they are easily detected in biological samples. The fluorogenic

XX protease indicators utilise high efficiency fluorophores and are able to

XX achieve a high degree of quenching while providing a strong signal when

XX the quench is released by cleavage of the peptide substrate. The high

XX signal allows detection of very low levels of protease activity. Thus the

XX fluorogenic protease indicators are particularly well suited for in situ

XX detection of protease activity. ABU60357-ABU60477 represent peptides use

XX to illustrate the method described in the disclosure of the invention

SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7

Db 1 YVHDAPV 7

RESULT 4

ID ADN88521

XX ADN88521 standard; peptide; 7 AA.

XX AC ADN88521;

XX 12-AUG-2004 (first entry)

DE Fluorogenic protease indicator peptide #217.  
KW fluorogenic; protease detection; protease inhibitor.  
XX Synthetic.

OS  
PN US2004096926-A1.  
XX

XX  
PD 20-MAY-2004.  
XX

XX  
PF 04-JUN-2001; 2001US-00874350.  
XX

XX  
PR 20-FEB-1997; 97US-00802981.  
XX

XX  
PR 20-FEB-1998; 98WO-US003000.  
XX

XX  
PR 10-SEP-1999; 99US-00394019.  
XX

XX  
PR 11-SEP-2000; 2000WO-US024882.  
XX

XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX

XX  
PI Packard BS, Komoriya A;  
XX

XX  
DR WPI; 2004-399235/37.  
XX

XX Fluorogenic composition useful for detecting protease activity and test  
PT substance modulating protease activity.  
XX

XX  
PS Claim 24; SEQ ID NO 217; 114pp; English.  
XX

CC The invention relates to a fluorogenic composition (I) for detecting the  
CC activity of a protease. (I) is useful for detecting the activity of a  
CC protease, which involves contacting the protease with (I), where the  
CC activity of protease is detected in a histological section, cell culture  
CC or tissue section. The cell suspension is derived from the biological  
CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
CC protease activity is detected by fluorescence microscopy, fluorescence  
CC microplate reader, absorption microscopy or confocal fluorescent microplate  
CC reader. (I) is useful for delivering a molecule into a cell, and for  
CC screening a test agent for the ability to modulate the activity of the  
CC protease. (I) is useful for detection and localisation of protease  
CC activity in biological samples. (I) also acts as a protease inhibitor,  
CC thus useful as protease inhibitors. (I) enables detection of the protease  
CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
CC represents a fluorogenic protease indicator peptide of the invention.  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
|||

Db 1 YVHDAVP 7  
|||

RESULT 5

ADN88514

ID ADN88514 standard; peptide; 7 AA.

XX  
AC ADN88514;

XX  
DT 12-AUG-2004 (first entry)

XX  
DE Fluorogenic protease indicator peptide #210.

XX fluorogenic; protease detection; protease inhibitor.  
XX  
OS Synthetic.  
XX  
PN US2004096926-A1.  
XX

PD 20-MAY-2004.

XX  
PF 04-JUN-2001; 2001US-00874350.  
XX

XX  
PR 20-FEB-1997; 97US-00802981.  
XX

XX  
PR 20-FEB-1998; 98WO-US003000.  
XX

XX  
PR 10-SEP-1999; 99US-00394019.  
XX

XX  
PR 11-SEP-2000; 2000WO-US024882.  
XX

XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX

XX  
PI Packard BS, Komoriya A;  
XX

XX  
DR WPI; 2004-399235/37.  
XX

XX Fluorogenic composition useful for detecting protease activity and test  
PT substance modulating protease activity.  
XX

XX  
PS Claim 1; SEQ ID NO 210; 114pp; English.  
XX

CC The invention relates to a fluorogenic composition (I) for detecting the  
CC activity of a protease. (I) is useful for detecting the activity of a  
CC protease, which involves contacting the protease with (I), where the  
CC activity of protease is detected in a histological section, cell culture  
CC or tissue section. The cell suspension is derived from the biological  
CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
CC protease activity is detected by fluorescence microscopy, fluorescence  
CC microplate reader, absorption microscopy or confocal fluorescent microplate  
CC reader. (I) is useful for delivering a molecule into a cell, and for  
CC screening a test agent for the ability to modulate the activity of the  
CC protease. (I) is useful for detection and localisation of protease  
CC activity in biological samples. (I) also acts as a protease inhibitor,  
CC thus useful as protease inhibitors. (I) enables detection of the protease  
CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
CC represents a fluorogenic protease indicator peptide of the invention.  
XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
|||

Db 1 YVHDAVP 7  
|||

RESULT 6

ADN88520

ID ADN88520 standard; peptide; 7 AA.

XX  
AC ADN88520;

XX  
DT 12-AUG-2004 (first entry)

XX  
DE Fluorogenic protease indicator peptide #216.

XX fluorogenic; protease detection; protease inhibitor.  
XX  
OS Synthetic.  
XX  
PN US2004096926-A1.  
XX

XX  
PD 20-MAY-2004.  
XX

XX  
PF 04-JUN-2001; 2001US-00874350.  
XX

XX  
PR 20-FEB-1997; 97US-00802981.  
XX

XX  
PR 20-FEB-1998; 98WO-US003000.  
XX

XX  
PR 10-SEP-1999; 99US-00394019.  
XX

XX  
PR 11-SEP-2000; 2000WO-US024882.  
XX



XX (ONCO-) ONCOIMMUNIN INC.  
 XX Packard BS, Komoriya A;  
 XX WPI; 2004-399235/37.  
 XX  
 XX Fluorogenic composition useful for detecting protease activity and test  
 XX substance modulating protease activity.  
 XX  
 XX Claim 24; SEQ ID NO 216; 114pp; English.  
 XX  
 XX The invention relates to a fluorogenic composition (I) for detecting the  
 XX activity of a protease. (I) is useful for detecting the activity of a  
 XX protease, which involves contacting the protease with (I), where the  
 XX activity of protease is detected in a histological section, cell culture  
 XX or tissue section. The cell suspension is derived from the biological  
 XX sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
 XX protease activity is detected by fluorescence microscopy, fluorescence  
 XX microplate reader, absorption spectroscopy or confocal fluorescent microplate  
 XX reader. (I) is useful for delivering a molecule into a cell, and for  
 XX screening a test agent for the ability to modulate the activity of the  
 XX protease. (I) is useful for detection and localisation of protease  
 XX activity in biological samples. (I) also acts as a protease inhibitor,  
 XX thus useful as protease inhibitors. (I) enables detection of the protease  
 XX activity, and provides a high intensity fluorescent signal at a visible  
 XX wavelength when they are digested by a protease. The present sequence  
 XX represents a fluorogenic protease indicator peptide of the invention.  
 XX  
 XX Sequence 7 AA;  
 XX  
 XX Query Match 100.0%; Score 40; DB 8; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 YVHDAVP 7  
 XX Db 1 YVHDAVP 7  
 XX  
 XX RESULT 7  
 XX AAR34855  
 XX ID AAR34855 standard; protein; 8 AA.  
 XX AC AAR34855;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX DT 14-JUL-1993 (first entry)  
 XX  
 XX IL-beta protease cleavage site peptide substrate.  
 XX  
 XX Interleukin; therapeutic; wound healing; treatment; arthritis;  
 XX autoimmune disease; radiation; side effects.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX FT Cleavage-site 3..6  
 XX FT /note= "IL-beta protease cleavage site"  
 XX  
 XX WO9305071-A1.  
 XX PN  
 XX 18-MAR-1993.  
 XX PD  
 XX 12-SEP-1991; 91WO-US006595.  
 XX PF  
 XX 30-AUG-1991; 91US-00750644.  
 XX PR  
 XX (IMV ) IMMUNEX CORP.  
 XX PA  
 XX Black RA, Sleath PR, Kronheim SR;  
 XX PI  
 XX

DR WPI; 1993-100924/12.  
 XX  
 XX New polypeptide having protease biological activity for interleukin 1-  
 XX beta - can form inhibitor compsn. and cpds. for treatment of arthritis,  
 XX auto-immune diseases, inflammation and radiation damage; also for wound  
 XX healing.  
 XX  
 XX Example; Page 39; 69pp; English.  
 XX  
 XX The sequence is that of a peptide corresponding to Tyr113 to Arg120 of  
 XX human precursor interleukin (IL)-1beta sequence which contains the  
 XX cleavage site (His115-Pro118) for IL-1beta protease. It shows a  
 XX reactivity of 2.40 relative to the peptide comprising amino acids Ala112-  
 XX Ser121 (AAR34851). (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 100.0%; Score 40; DB 2; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 YVHDAVP 7  
 XX Db 1 YVHDAVP 7  
 XX  
 XX RESULT 8  
 XX AAP80605  
 XX ID AAP80605 standard; protein; 10 AA.  
 XX AC AAP80605;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX DT 16-NOV-1990 (first entry)  
 XX  
 XX Sequence of AA positions 112 to 269 of pro human interleukin I beta (hIL-  
 XX 1-beta).  
 XX  
 XX Plasmid pDP506; pUC8; plasmid pDP516; haematopoiesis;  
 XX pUC9-hIL-1-beta-delta-AccI; Human IL-1-beta derivative.  
 XX  
 XX Homo sapiens.  
 XX  
 XX EP276778-A.  
 XX  
 XX 03-AUG-1988.  
 XX  
 XX 22-JAN-1988; 88EP-00100924.  
 XX  
 XX 27-JAN-1987; 87US-00006870.  
 XX 18-DEC-1987; 87US-00132185.  
 XX  
 XX (DUPO ) DU PONT DE NEMOURS & CO E.I.  
 XX (DUPO ) DU PONT MERCK PHARMACEUTICAL CO.  
 XX  
 XX Huang JJH;  
 XX  
 XX WPI; 1988-214198/31.  
 XX N-PSDB; AAN81008.  
 XX  
 XX Plasmid for expression of mature human interleukin 1 beta - comprising  
 XX DNA coding for aminoacid sequence 5 to 153 with alterations at N-  
 XX terminus.  
 XX  
 XX Disclosure; Fig 3; 12pp; English.  
 XX  
 XX The SQ in AAN81008 has an HgiAI site and there is a PstI site approx.150  
 XX nucleotides downstream from the pro hIL-1-beta coding sequence. To  
 XX construct pDP506, a 0.6 Kb restriction fragment was produced by digestion  
 XX of pUC9-pro hIL-1-beta-delta-AccI with HgiAI and PstI, and the 0.6 Kb  
 XX fragment contg. mature hIL-1-beta coding sequence was inserted into the  
 XX PstI site of pUC8. Plasmids of pDP516 series were produced by digesting  
 XX pDP506 with EcoRI and SalI to produce linear DNA, digesting this with

CC Bal31 exonuclease, filling in recessed 3' ends by Klenow reaction and  
 CC ligating the blunt ends with T4 DNA ligase to recircularise the DNA. The  
 CC pDP516 series are claimed. (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
 Db 2 YVHDAVP 8  
 |||||

## RESULT 9

AAR34851  
 ID AAR34851 standard; protein; 10 AA.

AC AAR34851;

DT 25-MAR-2003 (revised)

DT 14-JUL-1993 (first entry)

DE IL-beta protease cleavage site peptide substrate.

XX Interleukin; therapeutic; wound healing; treatment; arthritis;  
 KW autoimmune disease; radiation; side effects.  
 KW  
 XX Synthetic.

Key Location/Qualifiers  
 FT Cleavage-site 4..7 /note= "IL-beta protease cleavage site"  
 FT  
 FT

PN WO9305071-A1.

XX 18-MAR-1993.

XX 12-SEP-1991; 91WO-US006595.

XX 30-AUG-1991; 91US-00750644.

XX (IMMV ) IMMUNEX CORP.

XX Black RA, Sleath PR, Kronheim SR;

XX WPI; 1993-100924/12.

XX New polypeptide having protease biological activity for interleukin 1-  
 PT beta - can form inhibitor compsn. and cpds. for treatment of arthritis,  
 PT auto:immune diseases, inflammation and radiation damage; also for wound  
 PT healing.

XX Example; Page 37; 69pp; English.

XX The sequence is that of a peptide corresponding to Ala12 to Ser121 of  
 CC human precursor interleukin (IL)-beta sequence. This contains the IL-  
 CC beta protease cleavage site (His115-Pro118) for IL-beta protease.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
 Db 2 YVHDAVP 8  
 |||||

## RESULT 10

AAW93092  
 ID AAW93092 standard; peptide; 10 AA.

XX AAW93092;

DT 20-MAY-1999 (first entry)

XX Phosphinyloxymethyl ketone peptide substrate.

XX Phosphinyloxymethyl ketone; interleukine-lbeta converting enzyme;  
 KW inhibitor; protease; treatment; infectious disease; meningitis; colitis;  
 KW salpingitis; septic shock; respiratory disease; inflammatory condition;  
 KW arthritis; cholangitis; encephalitis; endocervicitis; hepatitis;  
 KW pancreatitis; reperfusion injury; immune-based disease; tumour;  
 KW multiple sclerosis; hypersensitivity; autoimmune disease.  
 XX Synthetic.

OS

XX Key Location/Qualifiers

XX Modified-site 1 /note= "labelled with TRITC (tetramethylrhodamine  
 FT isothiocyanate"  
 FT 11  
 FT Modified-site 11 /note= "C-terminal amidated"

XX US5843305-A.

XX 01-DEC-1998.

XX 06-FEB-1996; 96US-00597346.

XX 04-JUN-1993; 93US-00073219.

XX 25-MAY-1994; 94US-00248791.

XX (VERT-) VERTEX PHARM INC.

XX Speier G, Singh J, Dolle RE;

XX WPI; 1999-044629/04.

XX Peptidic phosphinyloxymethyl ketones - are interleukin-lbeta protease  
 PT inhibitors useful for treating, e.g. infectious diseases, septic shock  
 PT and respiratory diseases.

XX Example 19; Col 15-16; 11pp; English.

XX This invention describes novel peptidic phosphinyloxymethyl ketones of  
 CC formula: R1-(AA)n-NH-Y (I) where n = 0-4; Y = -C(R2)(CH2COR3)  
 CC (COCHR4OP(=O)R5R6); R2 = H or deuterium; R3 = OH, OR7, NR7OR8 or NR7R8;  
 CC R7,R8 = H, alkyl, cycloalkyl, etc.; R4 = H or lower alkyl; R5,R6 = H, OH,  
 CC alkyl, alkoxy or phenyloxy; AA = a group of formula (II), (1) or (6); R9  
 CC = (CR6R7)0-6-R10; R10 = R11; W, X = CH2 or O; R1 = R10-CO-; R11 = H,  
 CC alkyl, alkenyl, OH, benzyl, alkoxy, 2-(alkyloxy)ethoxy, 2-(alkyloxy)  
 CC aminoethyl, 2-(alkyloxy)-N-alkylaminoethyl, alkylacyloxy, alkylacyl,  
 CC halo, haloalkyl, guanidino, mono- or di-alkylguanidino,  
 CC alkylacylguanidino, amidino, mono- or di-alkylamidino, NH2, mono- or di-  
 CC -alkylamino, etc. Such ketones are inhibitors of interleukin-1 beta  
 CC protease and are useful for treating infectious diseases (e.g. meningitis  
 CC and salpingitis), septic shock, respiratory diseases, inflammatory  
 CC conditions (e.g. arthritis, cholangitis, colitis, encephalitis,  
 CC endocervicitis, hepatitis, pancreatitis and reperfusion injury), immune-  
 CC based diseases (e.g., hypersensitivity), autoimmune diseases (e.g.  
 CC multiple sclerosis), bond diseases and certain tumours

SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
 |||||

Db 2 YVHDAPV 8

RESULT 11  
AAB92087  
ID AAB92087 standard; peptide; 10 AA.  
XX  
AC AAB92087;  
XX  
DT 22-JUN-2001 (first entry)  
XX  
DE Interleukin (IL) and interleukin receptor protein peptide SEQ ID NO:1263.  
XX  
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX WO200069900-A2.  
XX  
XX 23-NOV-2000.  
XX  
XX 17-MAY-2000; 2000WO-US013576.  
XX  
XX 17-MAY-1999; 99US-0134406P.  
XX  
XX 10-SEP-1999; 99US-0153406P.  
XX  
XX 15-OCT-1999; 99US-0159783P.  
XX  
XX (CONJ-) CONJUCHEM INC.  
XX  
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
XX  
XX WPI; 2001-112059/12.  
XX  
XX Modifying and attaching therapeutic peptides to albumin prevents  
XX peptidase degradation, useful for increasing length of in vivo activity.  
XX  
XX Disclosure; Page 608; 733pp; English.  
XX  
XX The present invention describes a modified therapeutic peptide (I)  
XX comprising a therapeutically active amino acid region (III) and a  
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
XX a less therapeutically active amino acid region (IV), which covalently  
XX bonds with amino/hydroxyl/thiol groups on blood components to form a  
XX peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
XX factors and neurotransmitters, to protect them from peptidase activity in  
XX vivo for the treatment of various disorders. Endogenous therapeutic  
XX peptides are not suitable as drug candidates as they require frequent  
XX administration due to rapid degradation by peptidases in the body.  
XX Modifying and attaching therapeutic peptides to albumin prevents or  
XX reduces the action of peptidases to increase length of activity (half  
XX life) and specificity as bonding to large molecules decreases  
XX intracellular uptake and interference with physiological processes.  
XX AAB90829 to AAB92441 represent peptides which can be used in the  
XX exemplification of the present invention  
XX  
XX Sequence 10 AA;  
XX  
Query Match 100.0%; Score 40; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
DB 2 YVHDAPV 8  
|||||  
RESULT 12  
AAG94006  
ID AAG94006 standard; peptide; 10 AA.

XX AAG94006;  
XX  
XX 18-SEP-2001 (first entry)  
XX  
XX Human complementary peptide, SEQ ID NO: 200.  
XX  
XX Human, complementary peptide; ligand; drug discovery; drug design.  
XX  
XX Homo sapiens.  
XX  
XX WO200142277-A2.  
XX  
XX 14-JUN-2001.  
XX  
XX 13-DEC-2000; 2000WO-GB004776.  
XX  
XX 13-DEC-1999; 99GB-00029464.  
XX  
XX (PROT-) PROTEOM LTD.  
XX  
XX Roberts GW, Heal JR;  
XX  
XX WPI; 2001-408419/43.  
XX  
XX A set of peptide ligands consisting of specific complementary peptides to  
XX PT proteins encoded by genes of the human genome, useful in an assay for  
XX PT screening and identifying of one or more novel peptides which are drug  
XX PT candidates or pro-drugs.  
XX  
XX Example 4; Page 69; 646pp; English.  
XX  
XX The invention relates to a set of complementary peptide ligands generated  
XX CC from the human genome. The complementary peptides interact with their  
XX CC relevant target proteins encoded in the human genome. They can be used as  
XX CC reagents in drug discovery and as lead ligands to facilitate drug design  
XX CC and development. The present sequence is a complementary peptide provided  
XX CC in the specification  
XX  
XX Sequence 10 AA;  
XX  
Query Match 100.0%; Score 40; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
DB 2 YVHDAPV 8  
|||||  
RESULT 13  
ADE86218  
ID ADE86218 standard; peptide; 10 AA.  
XX  
XX ADE86218;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Interleukin-lbета (IL-lbета) protease assay substrate.  
XX  
XX antiarthritic; antirheumatic; cytostatic; antibacterial;  
XX immunosuppressive; antiinflammatory; osteopathic; respiratory;  
XX neuroprotective; hepatotropic; virucide; vasotropic; gastrointestinal;  
XX interleukin-lbета protease inhibitor;  
XX alpha-substituted methyl ketone compound; arthritis;  
XX rheumatoid arthritis; acute myelogenous leukaemia blast proliferation;  
XX infection; meningitis; salpingitis; septic shock; respiratory disease;  
XX inflammatory condition; encephalitis; cholangitis; colitis;  
XX endocervicitis; hepatitis; pancreatitis; reperfusion injury;  
XX immune-based disease; hypersensitivity; auto-immune disease;  
XX multiple sclerosis; bone disease; tumour; IL-lbета protease.  
XX  
XX Synthetic.

OS Unidentified.  
 XX US6576614-B1.  
 XX 10-JUN-2003.  
 PD 20-OCT-1999; 99US-00421954.  
 XX 29-APR-1993; 93US-00055051.  
 PR 12-JAN-1995; 95US-00371723.  
 PR 10-JUL-1996; 96US-00679350.  
 XX (VERT-) VERTEX PHARM INC.  
 XX Dolle RE, Osifo IK, Schmidt SJ, Hoyer DW, Ross TM;  
 PI Chaturvedula PV, Prouty CP, Awad MMA, Salvino JM, Rinker JM;  
 PI Lodge EP, Singh J, Ator MA;  
 XX WPI; 2004-030323/03.  
 DR Inhibition of interleukin-lbета protease activity useful for treating  
 PT e.g. arthritis involves the use of alpha substituted methyl ketone  
 PT compounds.  
 XX Example 71; SEQ ID NO 1; 20pp; English.  
 XX The invention describes a method of inhibiting interleukin-lbета protease  
 CC activity involving administration of alpha-substituted methyl ketone  
 CC compounds or their salts. The inhibition method is useful for treating  
 CC arthritis and rheumatoid arthritis; for suppressing acute myelogenous  
 CC leukaemia blast proliferation. Also for treating diseases or disorders  
 CC e.g. infections (such as meningitis and salpingitis); septic shock,  
 CC respiratory diseases, inflammatory conditions (e.g. encephalitis,  
 CC cholangitis, colitis, endocervicitis, hepatitis, pancreatitis and  
 CC reperfusion injury), immune-based diseases (e.g. hypersensitivity), auto-  
 CC immune diseases (e.g. multiple sclerosis), bone diseases and tumour. The  
 CC compound binds at the active site of IL-lbета protease and inhibits IL-  
 CC lbета protease activity. This is the amino acid sequence of an  
 CC interleukin-lbета (IL-lbета) protease assay peptide substrate.  
 XX Sequence 10 AA;  
 SQ  
 Query Match 100.0%; Score 40; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;  
 QY 1 YVHDAVP 7  
 DB 2 YVHDAVP 8  
 |||||  
 |||||  
 RESULT 14  
 AAW29953  
 ID AAW29953 standard; peptide; 14 AA.  
 XX AAW29953;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 16-MAR-1998 (first entry)  
 XX Cysteine protease Ich-1 candidate substrate #2.  
 DE  
 XX Cysteine protease Ich-1; neurodegenerative disease; stroke;  
 KW neuronal inflammation; inhibitor; substrate; polyhistidine tag;  
 KW interleukin-1-beta converting enzyme; ICE; N-His Ich-1.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "N-terminal acetyl"  
 FT 14  
 FT Modified-site 14  
 FT /note= "C-terminal amide"

XX WO9727220-A2.  
 XX 31-JUL-1997.  
 PD 28-JAN-1997; 97WO-US001485.  
 XX 29-JAN-1996; 96US-0052943.  
 PR 18-JUN-1996; 96US-00665643.  
 XX (BADI ) BASF AG.  
 PA (PARK ) PARKE-DAVIS.  
 XX Talanian RV, Ghayur T, Hodges JC;  
 PI WPI; 1997-393619/36.  
 DR New substrates and inhibitors for cysteine protease Ich-1 - used for  
 XX inhibiting, detecting or isolating Ich-1, e.g. for treating  
 PT neurodegenerative diseases, neuronal inflammation or stroke.  
 PT  
 XX Example 1; Page 26; 59pp; English.  
 PS To identify peptide substrates for Ich-1, candidate peptides were used in  
 CC in vitro proteolysis assays with recombinant Ich-1 protein. The human Ich  
 CC -1 enzyme was expressed recombinantly with an N-terminal polyhistidine  
 CC tag. The resulting enzyme, N-His Ich-1, contains Ich-1 amino acid  
 CC residues 167-435, with an initiator and polyhistidine tag fused to the  
 CC amino terminus. Peptides (AAW29952-58) corresponding to known or  
 CC suspected cleavage sites for interleukin-1-beta converting enzyme (ICE)  
 CC were tested as Ich-1 substrates. The sequence (AAW29952) corresponding to  
 CC amino acids 310-20 of human Ich-1 with a tryptophan residue at the  
 CC carboxy-terminus was cleaved at a rate significantly higher than the  
 CC other tested peptides. To determine the length dependence of peptide  
 CC cleavage by N-His Ich-1, a series of peptides (AAW29959-65) based on this  
 CC sequence but varying in length at the amino or carboxy termini were  
 CC tested in proteolysis assays. The results provide an optimal amino acid  
 CC sequence of VVAD. This sequence represents a generic formula for  
 CC compounds which act as inhibitors or substrates for the cysteine protease  
 CC Ich-1. The inhibitor compounds can be used to inhibit the proteolytic  
 CC activity of Ich-1 or to isolate Ich-1. They can be used in the treatment  
 CC of neurodegenerative diseases, such as Alzheimer's disease, neuronal  
 CC inflammation and stroke. The substrate compounds can be used to detect  
 CC the presence of Ich-1 in samples. (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 XX SQ Sequence 14 AA;  
 Query Match 100.0%; Score 40; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAVP 7  
 DB 4 YVHDAVP 10  
 |||||  
 |||||  
 RESULT 15  
 AAG73121  
 ID AAG73121 standard; peptide; 14 AA.  
 XX AAG73121;  
 AC  
 XX 14-AUG-2001 (first entry)  
 DT Protease binding site #55.  
 XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
 KW haemophilia.  
 XX Synthetic.  
 OS

PH Key Location/Qualifiers  
FT Modified-site 3 /label= Aib  
FT /note= "2-aminoisobutyric acid"  
XX WO200118238-A1.  
XX 15-MAR-2001.  
XX  
XX PF 11-SEP-2000; 2000WO-US024882.  
XX  
XX PR 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Komoriya A, Packard BS;  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
XX Disclosure; Page 24; 86pp; English.  
XX  
XX The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 100.0%; Score 40; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
DB 4 YVHDAPV 10  
|||||  
RESULT 16  
AAG73120  
ID AAG73120 standard; peptide; 14 AA.  
XX  
XX AAG73120;  
XX  
XX 14-AUG-2001 (first entry)  
XX  
XX Protease binding site #54.  
XX  
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
KW haemophilia.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 3 /label= Aib  
FT /note= "2-aminoisobutyric acid"  
XX WO200118238-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX PF 11-SEP-2000; 2000WO-US024882.  
XX  
XX PR 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Komoriya A, Packard BS;  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
XX Disclosure; Page 24; 86pp; English.  
XX  
XX The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 100.0%; Score 40; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
DB 4 YVHDAPV 10  
|||||  
RESULT 17  
AAG73119  
ID AAG73119 standard; peptide; 14 AA.  
XX  
XX AAG73119;  
XX  
XX 14-AUG-2001 (first entry)  
XX  
XX Protease binding site #53.  
XX  
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
KW haemophilia.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 3 /label= Aib  
FT /note= "2-aminoisobutyric acid"  
XX WO200118238-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX PF 11-SEP-2000; 2000WO-US024882.  
XX  
XX PR 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Komoriya A, Packard BS;  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT

PR 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Komoriya A, Packard BS;  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
XX Disclosure; Page 24; 86pp; English.  
XX  
XX The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 100.0%; Score 40; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
DB 4 YVHDAPV 10  
|||||  
RESULT 17  
AAG73119  
ID AAG73119 standard; peptide; 14 AA.  
XX  
XX AAG73119;  
XX  
XX 14-AUG-2001 (first entry)  
XX  
XX Protease binding site #53.  
XX  
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
KW haemophilia.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 3 /label= Aib  
FT /note= "2-aminoisobutyric acid"  
XX WO200118238-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX PF 11-SEP-2000; 2000WO-US024882.  
XX  
XX PR 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Komoriya A, Packard BS;  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT

PT samples.  
 XX Disclosure; Page 24; 86pp; English.  
 XX  
 CC The present invention describes fluorogenic compositions which can be  
 CC used for the detection of protease activity. This can be useful as an  
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
 CC thrombosis and arthritis. The fluorogenic compositions comprise a  
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
 CC peptide is cleaved by a protease and the fluorophores can then be  
 CC detected. The present sequence is one of the peptides described in the  
 CC exemplification of the invention  
 XX  
 XX Sequence 14 AA;  
 SQ

Query Match 100.0%; Score 40; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 4 YVHDAPV 10  
 |||||

RESULT 18  
 AAM50413  
 ID AAM50413 standard; peptide; 14 AA.  
 XX  
 AC AAM50413;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Tumour associated activatable guarding moiety.  
 XX  
 KW Magnetic resonance imaging; MRI; cancer; detection; contrasting agent;  
 KW tumour associated activatable guarding moiety; TAAGM.  
 XX  
 OS Synthetic.  
 XX  
 WO200182976-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 04-MAY-2001; 2001WO-US014470.  
 XX  
 PR 04-MAY-2000; 2000US-0201816P.  
 PR 17-NOV-2000; 2000US-00715859.  
 XX  
 PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.  
 XX  
 PI Meade TJ;  
 XX  
 WPI; 2002-075134/10.  
 XX  
 PT New magnetic resonance imaging contrast agents for detection of cancerous  
 PT cells and tissues.  
 XX  
 PS Disclosure; Page 27; 61pp; English.  
 XX  
 CC The present peptide is an example of a tumour associated activatable  
 CC guarding moiety (TAAGM) that is used in a preferred embodiment of the  
 CC invention. A claimed magnetic resonance imaging (MRI) contrast agent  
 CC composition comprises: a gadolinium (III) ion bound to a first chelator  
 CC such that the ion has coordination atoms in at least 7 of its  
 CC coordination sites; and a TAAGM covalently attached to the first chelator  
 CC which hinders the rapid exchange of water in the remaining coordination  
 CC sites of the Gd(III) ion. The novel MRI contrast agents can target  
 CC substances that are associated with cancer. By using a targeting moiety,  
 CC the MRI agents become more effective, discriminatory and selective with  
 CC regard to signal detection of disease pathology  
 XX  
 XX Sequence 14 AA;  
 SQ

Query Match 100.0%; Score 40; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 4 YVHDAPV 10  
 |||||

RESULT 19  
 ADN88359  
 ID ADN88359 standard; peptide; 14 AA.  
 XX  
 AC ADN88359;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Fluorogenic protease indicator peptide #55.  
 XX  
 KW fluorogenic; protease detection; protease inhibitor.  
 XX  
 OS Synthetic.  
 XX  
 US2004096926-A1.  
 XX  
 PD 20-MAY-2004.  
 XX  
 PF 04-JUN-2001; 2001US-00874350.  
 XX  
 PR 20-FEB-1997; 97US-00802981.  
 PR 20-FEB-1998; 98WO-US003000.  
 PR 10-SEP-1993; 93US-00394019.  
 PR 11-SEP-2000; 2000WO-US024882.  
 XX  
 PA (ONCO-) ONCOIMMUNIN INC.  
 XX  
 PI Packard BS, Komoriya A;  
 XX  
 WPI; 2004-399235/37.  
 XX  
 PT Fluorogenic composition useful for detecting protease activity and test  
 PT substance modulating protease activity.  
 XX  
 PS Disclosure; SEQ ID NO 55; 114pp; English.  
 XX  
 CC The invention relates to a fluorogenic composition (I) for detecting the  
 CC activity of a protease. (I) is useful for detecting the activity of a  
 CC protease, which involves contacting the protease with (I), where the  
 CC activity of protease is detected in a histological section, cell culture  
 CC or tissue section. The cell suspension is derived from the biological  
 CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
 CC protease activity is detected by fluorescence microscopy, fluorescence  
 CC microplate reader, absorption spectroscopy or confocal fluorescent microplate  
 CC reader. (I) is useful for delivering a molecule into a cell, and for  
 CC screening a test agent for the ability to modulate the activity of the  
 CC protease. (I) is useful for detection and localisation of protease  
 CC activity in biological samples. (I) also acts as a protease inhibitor,  
 CC thus useful as protease inhibitors. (I) enables detection of the protease  
 CC activity, and provides a high intensity fluorescent signal at a visible  
 CC wavelength when they are digested by a protease. The present sequence  
 CC represents a fluorogenic protease indicator peptide of the invention.  
 XX  
 XX Sequence 14 AA;  
 SQ

Query Match 100.0%; Score 40; DB 8; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 4 YVHDAPV 10  
 |||||

RESULT 20  
ADN88361  
ID ADN88361 standard; peptide; 14 AA.  
XX  
AC ADN88361;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Fluorogenic protease indicator peptide #57.  
XX  
KW fluorogenic; protease detection; protease inhibitor.  
XX  
OS Synthetic.  
XX  
PN US2004096926-A1.  
XX  
PD 20-MAY-2004.  
XX  
PF 04-JUN-2001; 2001US-00874350.  
XX  
PR 20-FEB-1997; 97US-00802981.  
PR 20-FEB-1998; 98WO-US003000.  
PR 10-SEP-1999; 99US-00394019.  
PR 11-SEP-2000; 2000WO-US024882.  
XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX  
PI Packard BS, Komoriya A;  
XX  
WPI; 2004-399235/37.  
XX  
PT Fluorogenic composition useful for detecting protease activity and test substance modulating protease activity.  
XX  
PS Disclosure; SEQ ID NO 57; 114pp; English.  
XX  
CC The invention relates to a fluorogenic composition (I) for detecting the activity of a protease. (I) is useful for detecting the activity of a protease, which involves contacting the protease with (I), where the activity of protease is detected in a histological section, cell culture or tissue section. The cell suspension is derived from the biological sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The protease activity is detected by fluorescence microscopy, fluorescence microplate reader, absorption spectroscopy or confocal fluorescent microplate reader. (I) is useful for delivering a molecule into a cell, and for screening a test agent for the ability to modulate the activity of the protease. (I) is useful for detection and localisation of protease activity in biological samples. (I) also acts as a protease inhibitor, thus useful as protease inhibitors. (I) enables detection of the protease activity, and provides a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The present sequence represents a fluorogenic protease indicator peptide of the invention.

Query Match 100.0%; Score 40; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
DB 4 YVHDAVP 10

RESULT 21  
ADN88360  
ID ADN88360 standard; peptide; 14 AA.  
XX  
AC ADN88360;  
XX  
DT 12-AUG-2004 (first entry)

XX  
DE Fluorogenic protease indicator peptide #56.  
XX  
KW fluorogenic; protease detection; protease inhibitor.  
XX  
OS Synthetic.  
XX  
PN US2004096926-A1.  
XX  
PD 20-MAY-2004.  
XX  
PF 04-JUN-2001; 2001US-00874350.  
XX  
PR 20-FEB-1997; 97US-00802981.  
PR 20-FEB-1998; 98WO-US003000.  
PR 10-SEP-1999; 99US-00394019.  
PR 11-SEP-2000; 2000WO-US024882.  
XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX  
PI Packard BS, Komoriya A;  
XX  
WPI; 2004-399235/37.  
XX  
PT Fluorogenic composition useful for detecting protease activity and test substance modulating protease activity.  
XX  
PS Disclosure; SEQ ID NO 56; 114pp; English.  
XX  
CC The invention relates to a fluorogenic composition (I) for detecting the activity of a protease. (I) is useful for detecting the activity of a protease, which involves contacting the protease with (I), where the activity of protease is detected in a histological section, cell culture or tissue section. The cell suspension is derived from the biological sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The protease activity is detected by fluorescence microscopy, fluorescence microplate reader, absorption spectroscopy or confocal fluorescent microplate reader. (I) is useful for delivering a molecule into a cell, and for screening a test agent for the ability to modulate the activity of the protease. (I) is useful for detection and localisation of protease activity in biological samples. (I) also acts as a protease inhibitor, thus useful as protease inhibitors. (I) enables detection of the protease activity, and provides a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The present sequence represents a fluorogenic protease indicator peptide of the invention.

Query Match 100.0%; Score 40; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
DB 4 YVHDAVP 10

RESULT 22  
ADN88522  
ID ADN88522 standard; peptide; 14 AA.  
XX  
AC ADN88522;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Fluorogenic protease indicator peptide #218.  
XX  
KW fluorogenic; protease detection; protease inhibitor.  
XX  
OS Synthetic.  
XX  
PN US2004096926-A1.





PI Komoriya A, Packard BS;  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
XX Disclosure; Page 24; 86pp; English.  
XX  
XX The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
XX  
SQ Sequence 16 AA;  
Query Match 100.0%; Score 40; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAVP 7  
Db |||||  
5 YVHDAVP 11  
RESULT 25  
AAG73123  
ID AAG73123 standard; peptide; 16 AA.  
XX  
XX AAG73123;  
XX  
XX 14-AUG-2001 (first entry)  
XX  
XX Protease binding site #57.  
XX  
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
KW haemophilia.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 3 /label= Aib  
FT FT /note= "2-aminoisobutyric acid"  
XX  
XX WO200118238-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX 11-SEP-2000; 2000WO-US024882.  
XX  
XX 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Komoriya A, Packard BS;  
XX  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
XX Disclosure; Page 24; 86pp; English.  
XX  
XX

CC The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
XX  
SQ Sequence 16 AA;  
Query Match 100.0%; Score 40; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAVP 7  
Db |||||  
5 YVHDAVP 11  
RESULT 26  
AAG73122  
ID AAG73122 standard; peptide; 16 AA.  
XX  
XX AAG73122;  
XX  
XX 14-AUG-2001 (first entry)  
XX  
XX Protease binding site #56.  
XX  
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
KW haemophilia.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 3 /label= Aib  
FT FT /note= "2-aminoisobutyric acid"  
XX  
XX WO200118238-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX 11-SEP-2000; 2000WO-US024882.  
XX  
XX 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Komoriya A, Packard BS;  
XX  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
XX Disclosure; Page 24; 86pp; English.  
XX  
XX The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
XX  
SQ Sequence 16 AA;  
Query Match 100.0%; Score 40; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAVP 7  
Db |||||  
5 YVHDAVP 11  
RESULT 26  
AAG73122  
ID AAG73122 standard; peptide; 16 AA.  
XX  
XX AAG73122;  
XX  
XX 14-AUG-2001 (first entry)  
XX  
XX Protease binding site #56.  
XX  
XX Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
KW haemophilia.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Modified-site 3 /label= Aib  
FT FT /note= "2-aminoisobutyric acid"  
XX  
XX WO200118238-A1.  
XX  
XX 15-MAR-2001.  
XX  
XX 11-SEP-2000; 2000WO-US024882.  
XX  
XX 10-SEP-1999; 99US-00394019.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Komoriya A, Packard BS;  
XX  
XX WPI; 2001-389573/41.  
XX  
XX New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
XX Disclosure; Page 24; 86pp; English.  
XX  
XX The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
XX  
SQ Sequence 16 AA;

Query Match 100.0%; Score 40; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
Db 5 YVHDAVP 11

RESULT 27  
ADN8518  
ID ADN8518 standard; peptide; 16 AA.

XX AC ADN8518;  
XX DT 12-AUG-2004 (first entry)

XX DE Fluorogenic protease indicator peptide #214.

XX KW fluorogenic; protease detection; protease inhibitor.

XX OS Synthetic.

XX PN US2004096926-A1.

XX PD 20-MAY-2004.

XX PF 04-JUN-2001; 2001US-00874350.

XX PR 20-FEB-1997; 97US-00802981.

XX PR 20-FEB-1998; 98WO-US003000.

XX PR 10-SEP-1999; 99US-00394019.

XX PR 11-SEP-2000; 2000WO-US024882.

XX PA (ONCO-) ONCOIMMUNIN INC.

XX PI Packard BS, Komoriya A;

XX DR WPI; 2004-399235/37.

XX PT Fluorogenic composition useful for detecting protease activity and test substance modulating protease activity.

XX PS Claim 21; SEQ ID NO 214; 114pp; English.

XX SQ The invention relates to a fluorogenic composition (I) for detecting the activity of a protease. (I) is useful for detecting the activity of a protease, which involves contacting the protease with (I), where the activity of protease is detected in a histological section, cell culture or tissue section. The cell suspension is derived from the biological sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The protease activity is detected by fluorescence microscopy, fluorescence microplate reader, absorption microplate reader, flow cytometry, fluorometry, absorption spectroscopy or confocal fluorescent microplate reader. (I) is useful for delivering a molecule into a cell, and for screening a test agent for the ability to modulate the activity of the protease. (I) is useful for detection and localisation of protease activity in biological samples. (I) also acts as a protease inhibitor, thus useful as protease inhibitors. (I) enables detection of the protease activity, and provides a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The present sequence represents a fluorogenic protease indicator peptide of the invention.

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 40; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.28; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
Db 4 YVHDAVP 10

RESULT 28

ADN8362  
ID ADN8362 standard; peptide; 16 AA.

XX AC ADN8362;

XX DT 12-AUG-2004 (first entry)

XX DE Fluorogenic protease indicator peptide #58.

XX KW fluorogenic; protease detection; protease inhibitor.

XX OS Synthetic.

XX PN US2004096926-A1.

XX PD 20-MAY-2004.

XX PF 04-JUN-2001; 2001US-00874350.

XX PR 20-FEB-1997; 97US-00802981.

XX PR 20-FEB-1998; 98WO-US003000.

XX PR 10-SEP-1999; 99US-00394019.

XX PR 11-SEP-2000; 2000WO-US024882.

XX PA (ONCO-) ONCOIMMUNIN INC.

XX PI Packard BS, Komoriya A;

XX DR WPI; 2004-399235/37.

XX PT Fluorogenic composition useful for detecting protease activity and test substance modulating protease activity.

XX PS Disclosure; SEQ ID NO 58; 114pp; English.

XX SQ The invention relates to a fluorogenic composition (I) for detecting the activity of a protease. (I) is useful for detecting the activity of a protease, which involves contacting the protease with (I), where the activity of protease is detected in a histological section, cell culture or tissue section. The cell suspension is derived from the biological sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The protease activity is detected by fluorescence microscopy, fluorescence microplate reader, absorption microplate reader, flow cytometry, fluorometry, absorption spectroscopy or confocal fluorescent microplate reader. (I) is useful for delivering a molecule into a cell, and for screening a test agent for the ability to modulate the activity of the protease. (I) is useful for detection and localisation of protease activity in biological samples. (I) also acts as a protease inhibitor, thus useful as protease inhibitors. (I) enables detection of the protease activity, and provides a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The present sequence represents a fluorogenic protease indicator peptide of the invention.

XX SQ Sequence 16 AA;

Query Match 100.0%; Score 40; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
Db 5 YVHDAVP 11

RESULT 29

ADN8523  
ID ADN8523 standard; peptide; 16 AA.

XX AC ADN8523;

XX DT 12-AUG-2004 (first entry)

XX DE Fluorogenic protease indicator peptide #219.  
XX KW fluorogenic; protease detection; protease inhibitor.  
XX OS Synthetic.  
XX PN US2004096926-A1.  
XX XX  
XX PD 20-MAY-2004.  
XX XX  
XX PF 04-JUN-2001; 2001US-00874350.  
XX XX  
XX PR 20-FEB-1997; 97US-00802981.  
XX PR 20-FEB-1998; 98WO-US003000.  
XX PR 10-SEP-1999; 99US-00394019.  
XX PR 11-SEP-2000; 2000WO-US024882.  
XX XX  
XX PA (ONCO-) ONCOIMMUNIN INC.  
XX XX  
XX PI Packard BS, Komoriya A;  
XX XX WPI; 2004-399235/37.  
XX XX  
XX PT Fluorogenic composition useful for detecting protease activity and test  
XX PT substance modulating protease activity.  
XX PS Disclosure; SEQ ID NO 219; 114pp; English.  
XX XX  
XX CC The invention relates to a fluorogenic composition (I) for detecting the  
XX CC activity of a protease. (I) is useful for detecting the activity of a  
XX CC protease, which involves contacting the protease with (I), where the  
XX CC activity of protease is detected in a histological section, cell culture  
XX CC or tissue section. The cell suspension is derived from the biological  
XX CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
XX CC protease activity is detected by fluorescence microscopy, fluorescence  
XX CC microplate reader, absorption microplate reader, flow cytometry,  
XX CC fluorometry, absorption spectroscopy or confocal fluorescent microplate  
XX CC reader. (I) is useful for delivering a molecule into a cell, and for  
XX CC screening a test agent for the ability to modulate the activity of the  
XX CC protease. (I) is useful for detection and localisation of protease  
XX CC activity in biological samples. (I) also acts as a protease inhibitor,  
XX CC thus useful as protease inhibitors. (I) enables detection of the protease  
XX CC activity, and provides a high intensity fluorescent signal at a visible  
XX CC wavelength when they are digested by a protease. The present sequence  
XX CC represents a fluorogenic protease indicator peptide of the invention.  
XX XX  
XX SQ Sequence 16 AA;  
XX  
Query Match 100.0%; Score 40; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAVP 7  
DB 5 YVHDAVP 11  
RESULT 30  
ID ADN88363  
ADN88363 standard; peptide; 16 AA.  
XX AC  
XX ADN88363;  
XX XX  
XX DT 12-AUG-2004 (first entry)  
XX XX  
XX DE Fluorogenic protease indicator peptide #59.  
XX KW fluorogenic; protease detection; protease inhibitor.  
XX OS Synthetic.  
XX XX  
XX PN US2004096926-A1.  
XX XX

XX PD 20-MAY-2004.  
XX XX  
XX PF 04-JUN-2001; 2001US-00874350.  
XX XX  
XX PR 20-FEB-1997; 97US-00802981.  
XX PR 20-FEB-1998; 98WO-US003000.  
XX PR 10-SEP-1999; 99US-00394019.  
XX PR 11-SEP-2000; 2000WO-US024882.  
XX XX  
XX PA (ONCO-) ONCOIMMUNIN INC.  
XX XX  
XX PI Packard BS, Komoriya A;  
XX XX WPI; 2004-399235/37.  
XX XX  
XX PT Fluorogenic composition useful for detecting protease activity and test  
XX PT substance modulating protease activity.  
XX PS Disclosure; SEQ ID NO 59; 114pp; English.  
XX XX  
XX CC The invention relates to a fluorogenic composition (I) for detecting the  
XX CC activity of a protease. (I) is useful for detecting the activity of a  
XX CC protease, which involves contacting the protease with (I), where the  
XX CC activity of protease is detected in a histological section, cell culture  
XX CC or tissue section. The cell suspension is derived from the biological  
XX CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
XX CC protease activity is detected by fluorescence microscopy, fluorescence  
XX CC microplate reader, absorption microplate reader, flow cytometry,  
XX CC fluorometry, absorption spectroscopy or confocal fluorescent microplate  
XX CC reader. (I) is useful for delivering a molecule into a cell, and for  
XX CC screening a test agent for the ability to modulate the activity of the  
XX CC protease. (I) is useful for detection and localisation of protease  
XX CC activity in biological samples. (I) also acts as a protease inhibitor,  
XX CC thus useful as protease inhibitors. (I) enables detection of the protease  
XX CC activity, and provides a high intensity fluorescent signal at a visible  
XX CC wavelength when they are digested by a protease. The present sequence  
XX CC represents a fluorogenic protease indicator peptide of the invention.  
XX XX  
XX SQ Sequence 16 AA;  
XX  
Query Match 100.0%; Score 40; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAVP 7  
DB 5 YVHDAVP 11  
RESULT 31  
ADN88364  
ID ADN88364 standard; peptide; 16 AA.  
XX AC  
XX ADN88364;  
XX XX  
XX DT 12-AUG-2004 (first entry)  
XX XX  
XX DE Fluorogenic protease indicator peptide #60.  
XX KW fluorogenic; protease detection; protease inhibitor.  
XX OS Synthetic.  
XX XX  
XX PN US2004096926-A1.  
XX XX  
XX PD 20-MAY-2004.  
XX XX  
XX PF 04-JUN-2001; 2001US-00874350.  
XX XX  
XX PR 20-FEB-1997; 97US-00802981.  
XX PR 20-FEB-1998; 98WO-US003000.  
XX PR 10-SEP-1999; 99US-00394019.  
XX PR 11-SEP-2000; 2000WO-US024882.



PI Komoriya A, Packard BS;  
DR WPI; 2001-389573/41.  
XX  
PT New fluorogenic compositions whose fluorescence level increases in the  
PT presence of active proteases, useful for detecting and localizing  
PT protease activity in biological samples, particularly in frozen tissue  
PT samples.  
XX  
PS Disclosure; Page 24; 86pp; English.  
XX  
XX The present invention describes fluorogenic compositions which can be  
CC used for the detection of protease activity. This can be useful as an  
CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
CC thrombosis and arthritis. The fluorogenic compositions comprise a  
CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
CC peptide is cleaved by a protease and the fluorophores can then be  
CC detected. The present sequence is one of the peptides described in the  
CC exemplification of the invention  
XX  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 40; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
Db 6 YVHDAPV 12  
|||||  
RESULT 34  
ABU64171  
ID ABU64171 standard; peptide; 17 AA.  
XX  
AC ABU64171;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Caspase preferred ligand #4.  
XX  
XX Caspase; cellular cytotoxicity; protease substrate; disease pathogenesis;  
KW vaccine; immunotherapy.  
XX  
OS Unidentified.  
XX  
XX WO2003084333-A1.  
XX  
PD 16-OCT-2003.  
XX  
XX 29-JAN-2003; 2003WO-US002583.  
XX  
XX 29-JAN-2002; 2002US-0353112P.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Packard BS, Brown MJ, Feinberg M, Liu L, Silvestri G;  
PI Charrondi A, Komoriya A;  
PI WPI; 2003-788536/74.  
XX  
XX Detecting cell-mediated cytotoxicity, useful e.g. for optimizing  
PT vaccinating antigens, by determining activity of an apoptotic pathway,  
PT specifically activated caspase.  
XX  
XX Disclosure; Page 4; Opp; English.  
XX  
XX The present invention relates to a method for detecting cell-mediated  
CC cytotoxic activity, which comprises co-incubating target cells and  
CC cytotoxic effector cells then detecting activity of an apoptotic pathway  
CC in the target cells as an indication that the effector cells are active  
CC against the target cells. The method is used to study cytotoxic T  
CC lymphocyte (CTL)-mediated killing of target cells, e.g. for studying

CC pathogenesis of infectious diseases, screening for agents that induce a  
CC CTL response against specific antigens, optimisation of antigens for use  
CC in vaccines (or for quality control in vaccines), to detect retention of  
CC immunity, to test for exposure to an antigen and to determine if a tissue  
CC or organ intended for transplantation will elicit a cellular immune  
CC response in a host. The present sequence is a peptide used to demonstrate  
XX the method of the invention  
SQ Sequence 17 AA;  
Query Match 100.0%; Score 40; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
Db 5 YVHDAPV 11  
|||||  
RESULT 35  
ADN88365  
ID ADN88365 standard; peptide; 17 AA.  
XX  
AC ADN88365;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
XX Fluorogenic protease indicator peptide #61.  
XX  
XX fluorogenic; protease detection; protease inhibitor.  
XX  
XX Synthetic.  
XX  
XX US2004096926-A1.  
XX  
XX 20-MAY-2004.  
XX  
XX 04-JUN-2001; 2001US-00874350.  
XX  
XX 20-FEB-1997; 97US-00802981.  
PR 20-FEB-1998; 98WO-US003000.  
PR 10-SEP-1999; 99US-00394019.  
PR 11-SEP-2000; 2000WO-US024882.  
XX  
XX (ONCO-) ONCOIMMUNIN INC.  
XX  
XX Packard BS, Komoriya A;  
PI WPI; 2004-399235/37.  
XX  
XX Fluorogenic composition useful for detecting protease activity and test  
PT substance modulating protease activity.  
XX  
XX Disclosure; SEQ ID NO 61; 114pp; English.  
XX  
XX The invention relates to a fluorogenic composition (I) for detecting the  
CC activity of a protease. (I) is useful for detecting the activity of a  
CC protease, which involves contacting the protease with (I), where the  
CC activity of protease is detected in a histological section, cell culture  
CC or tissue section. The cell suspension is derived from the biological  
CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
CC protease activity is detected by fluorescence microscopy, fluorescence  
CC microplate reader, absorption microscopy or confocal fluorescence  
CC fluorometry, absorption spectroscopy or confocal fluorescent microplate  
CC reader. (I) is useful for delivering a molecule into a cell, and for  
CC screening a test agent for the ability to modulate the activity of the  
CC protease. (I) is useful for detection and localisation of protease  
CC activity in biological samples. (I) also acts as a protease inhibitor,  
CC thus useful as protease inhibitors. (I) enables detection of the protease  
CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
XX represents a fluorogenic protease indicator peptide of the invention.

```
SQ Sequence 17 AA;
Query Match 100.0%; Score 40; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
    |||||
Db 6 YVHDAPV 12

RESULT 36
ADN88366
ID ADN88366 standard; peptide; 17 AA.
AC ADN88366;
XX
XX
XX
XX
XX 12-AUG-2004 (first entry)
XX
XX Fluorogenic protease indicator peptide #62.
XX
XX fluorogenic; protease detection; protease inhibitor.
XX Synthetic.
XX
XX US2004096926-A1.
XX
XX 20-MAY-2004.
XX
XX 04-JUN-2001; 2001US-00874350.
XX
XX 20-FEB-1997; 97US-00802981.
XX 20-FEB-1998; 98WO-US003000.
XX 10-SEP-1999; 99US-00394019.
XX 11-SEP-2000; 2000WO-US024882.
XX
XX (ONCO-) ONCOIMMUNIN INC.
XX
XX Packard BS, Komoriya A;
XX
XX WPI; 2004-399235/37.
XX
XX Fluorogenic composition useful for detecting protease activity and test
XX substance modulating protease activity.
XX
XX Disclosure; SEQ ID NO 62; 114pp; English.
XX
XX The invention relates to a fluorogenic composition (I) for detecting the
XX activity of a protease. (I) is useful for detecting the activity of a
XX protease, which involves contacting the protease with (I), where the
XX activity of protease is detected in a histological section, cell culture
XX or tissue section. The cell suspension is derived from the biological
XX sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The
XX protease activity is detected by fluorescence microscopy, fluorescence
XX microplate reader, absorption microplate reader, flow cytometry,
XX fluorometry, absorption spectroscopy or confocal fluorescent microplate
XX reader. (I) is useful for delivering a molecule into a cell, and for
XX screening a test agent for the ability to modulate the activity of the
XX protease. (I) is useful for detection and localisation of protease
XX activity in biological samples. (I) also acts as a protease inhibitor,
XX thus useful as protease inhibitors. (I) enables detection of the protease
XX activity, and provides a high intensity fluorescent signal at a visible
XX wavelength when they are digested by a protease. The present sequence
XX represents a fluorogenic protease indicator peptide of the invention.
XX
XX Sequence 17 AA;
Query Match 100.0%; Score 40; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
    |||||
Db 6 YVHDAPV 12

RESULT 37
ADN88368
ID ADN88368 standard; peptide; 17 AA.
AC ADN88368;
XX
XX
XX 12-AUG-2004 (first entry)
XX
XX Fluorogenic protease indicator peptide #64.
XX
XX fluorogenic; protease detection; protease inhibitor.
XX Synthetic.
XX
XX US2004096926-A1.
XX
XX 20-MAY-2004.
XX
XX 04-JUN-2001; 2001US-00874350.
XX
XX 20-FEB-1997; 97US-00802981.
XX 20-FEB-1998; 98WO-US003000.
XX 10-SEP-1999; 99US-00394019.
XX 11-SEP-2000; 2000WO-US024882.
XX
XX (ONCO-) ONCOIMMUNIN INC.
XX
XX Packard BS, Komoriya A;
XX
XX WPI; 2004-399235/37.
XX
XX Fluorogenic composition useful for detecting protease activity and test
XX substance modulating protease activity.
XX
XX Disclosure; SEQ ID NO 64; 114pp; English.
XX
XX The invention relates to a fluorogenic composition (I) for detecting the
XX activity of a protease. (I) is useful for detecting the activity of a
XX protease, which involves contacting the protease with (I), where the
XX activity of protease is detected in a histological section, cell culture
XX or tissue section. The cell suspension is derived from the biological
XX sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The
XX protease activity is detected by fluorescence microscopy, fluorescence
XX microplate reader, absorption microplate reader, flow cytometry,
XX fluorometry, absorption spectroscopy or confocal fluorescent microplate
XX reader. (I) is useful for delivering a molecule into a cell, and for
XX screening a test agent for the ability to modulate the activity of the
XX protease. (I) is useful for detection and localisation of protease
XX activity in biological samples. (I) also acts as a protease inhibitor,
XX thus useful as protease inhibitors. (I) enables detection of the protease
XX activity, and provides a high intensity fluorescent signal at a visible
XX wavelength when they are digested by a protease. The present sequence
XX represents a fluorogenic protease indicator peptide of the invention.
XX
XX Sequence 17 AA;
Query Match 100.0%; Score 40; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
    |||||
Db 6 YVHDAPV 12

RESULT 38
ADN88367
ID ADN88367 standard; peptide; 17 AA.
AC ADN88367;
XX
```

XX DT 12-AUG-2004 (first entry)  
XX DE Fluorogenic protease indicator peptide #63.  
XX KW fluorogenic; protease detection; protease inhibitor.  
XX OS Synthetic.  
XX PN US2004096926-A1.  
XX PD 20-MAY-2004.  
XX PF 04-JUN-2001; 2001US-00874350.  
XX PR 20-FEB-1997; 97US-00802981.  
XX PR 20-FEB-1998; 98WO-US003000.  
XX PR 10-SEP-1999; 99US-00394019.  
XX PR 11-SEP-2000; 2000WO-US024882.  
XX PA (ONCO-) ONCOIMMUNIN INC.  
XX PI Packard BS, Komoriya A;  
XX DR WPI; 2004-399235/37.  
XX PT Fluorogenic composition useful for detecting protease activity and test  
XX PT substance modulating protease activity.  
XX PS Disclosure; SEQ ID NO 63; 114pp; English.  
XX CC The invention relates to a fluorogenic composition (I) for detecting the  
XX CC activity of a protease. (I) is useful for detecting the activity of a  
XX CC protease, which involves contacting the protease with (I), where the  
XX CC activity of protease is detected in a histological section, cell culture  
XX CC or tissue section. The cell suspension is derived from the biological  
XX CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
XX CC protease activity is detected by fluorescence microscopy, fluorescence  
XX CC microplate reader, absorption spectroscopy or confocal fluorescent microplate  
XX CC reader. (I) is useful for delivering a molecule into a cell, and for  
XX CC screening a test agent for the ability to modulate the activity of the  
XX CC protease. (I) is useful for detection and localisation of protease  
XX CC activity in biological samples. (I) also acts as a protease inhibitor,  
XX CC thus useful as protease inhibitors. (I) enables detection of the protease  
XX CC activity, and provides a high intensity fluorescent signal at a visible  
XX CC wavelength when they are digested by a protease. The present sequence  
XX CC represents a fluorogenic protease indicator peptide of the invention.  
XX SQ Sequence 17 AA;  
Query Match 100.0%; Score 40; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
Db 6 YVHDAPV 12  
RESULT 39  
ADN88369  
ID ADN88369 standard; peptide; 17 AA.  
XX AC ADN88369;  
XX DT 12-AUG-2004 (first entry)  
XX DE Fluorogenic protease indicator peptide #63.  
XX KW fluorogenic; protease detection; protease inhibitor.  
XX OS Synthetic.

XX PN US2004096926-A1.  
XX PD 20-MAY-2004.  
XX PF 04-JUN-2001; 2001US-00874350.  
XX PR 20-FEB-1997; 97US-00802981.  
XX PR 20-FEB-1998; 98WO-US003000.  
XX PR 10-SEP-1999; 99US-00394019.  
XX PR 11-SEP-2000; 2000WO-US024882.  
XX PA (ONCO-) ONCOIMMUNIN INC.  
XX PI Packard BS, Komoriya A;  
XX DR WPI; 2004-399235/37.  
XX PT Fluorogenic composition useful for detecting protease activity and test  
XX PT substance modulating protease activity.  
XX PS Disclosure; SEQ ID NO 65; 114pp; English.  
XX CC The invention relates to a fluorogenic composition (I) for detecting the  
XX CC activity of a protease. (I) is useful for detecting the activity of a  
XX CC protease, which involves contacting the protease with (I), where the  
XX CC activity of protease is detected in a histological section, cell culture  
XX CC or tissue section. The cell suspension is derived from the biological  
XX CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
XX CC protease activity is detected by fluorescence microscopy, fluorescence  
XX CC microplate reader, absorption spectroscopy or confocal fluorescent microplate  
XX CC reader. (I) is useful for delivering a molecule into a cell, and for  
XX CC screening a test agent for the ability to modulate the activity of the  
XX CC protease. (I) is useful for detection and localisation of protease  
XX CC activity in biological samples. (I) also acts as a protease inhibitor,  
XX CC thus useful as protease inhibitors. (I) enables detection of the protease  
XX CC activity, and provides a high intensity fluorescent signal at a visible  
XX CC wavelength when they are digested by a protease. The present sequence  
XX CC represents a fluorogenic protease indicator peptide of the invention.  
XX SQ Sequence 17 AA;  
Query Match 100.0%; Score 40; DB 8; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.3;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
Db 6 YVHDAPV 12  
RESULT 40  
AAG73237  
ID AAG73237 standard; peptide; 18 AA.  
XX AC AAG73237;  
XX DT 14-AUG-2001 (first entry)  
XX DE Protease binding site #171.  
XX KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
XX KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
XX KW haemophilia.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT Modified-site 1  
XX FT /label= OTHER  
XX FT /note= "modified by fluorophore"





CC used for the detection of protease activity. This can be useful as an  
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
 CC thrombosis and arthritis. The fluorogenic compositions comprise a  
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
 CC peptide is cleaved by a protease and the fluorophores can then be  
 CC detected. The present sequence is one of the peptides described in the  
 CC exemplification of the invention

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 |||||  
 Db 6 YVHDAPV 12

RESULT 43

AAG73126  
 ID AAG73126 standard; peptide; 18 AA.

AC AAG73126;

DT 14-AUG-2001 (first entry)

DE Protease binding site #60.

KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
 KW haemophilia.

OS Synthetic.

PH Key Location/Qualifiers  
 FT Modified-site 3

FT /label= Aib  
 FT /note= "2-aminoisobutyric acid"

PN WO200118238-A1.

PD 15-MAR-2001.

PF 11-SEP-2000; 2000WO-US024882.

PR 10-SEP-1999; 99US-00394019.

PA (ONCO-) ONCOIMMUNIN INC.

PI Komoriya A, Packard BS;

DR WPI; 2001-389573/41.

XX New fluorogenic compositions whose fluorescence level increases in the  
 PT presence of active proteases, useful for detecting and localizing  
 PT protease activity in biological samples, particularly in frozen tissue  
 PT samples.

XX PS Disclosure; Page 24; 86pp; English.

XX The present invention describes fluorogenic compositions which can be  
 CC used for the detection of protease activity. This can be useful as an  
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
 CC thrombosis and arthritis. The fluorogenic compositions comprise a  
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
 CC peptide is cleaved by a protease and the fluorophores can then be  
 CC detected. The present sequence is one of the peptides described in the  
 CC exemplification of the invention

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 |||||  
 Db 6 YVHDAPV 12

RESULT 44

AAG73236  
 ID AAG73236 standard; peptide; 18 AA.

AC AAG73236;

DT 14-AUG-2001 (first entry)

DE Protease binding site #170.

KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
 KW haemophilia.

OS Synthetic.

PH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= OTHER  
 FT /note= "modified by fluorophore"

PN WO200118238-A1.

PD 15-MAR-2001.

PF 11-SEP-2000; 2000WO-US024882.

PR 10-SEP-1999; 99US-00394019.

PA (ONCO-) ONCOIMMUNIN INC.

PI Komoriya A, Packard BS;

DR WPI; 2001-389573/41.

XX New fluorogenic compositions whose fluorescence level increases in the  
 PT presence of active proteases, useful for detecting and localizing  
 PT protease activity in biological samples, particularly in frozen tissue  
 PT samples.

XX PS Disclosure; Page 29; 86pp; English.

XX The present invention describes fluorogenic compositions which can be  
 CC used for the detection of protease activity. This can be useful as an  
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
 CC thrombosis and arthritis. The fluorogenic compositions comprise a  
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
 CC peptide is cleaved by a protease and the fluorophores can then be  
 CC detected. The present sequence is one of the peptides described in the  
 CC exemplification of the invention

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 |||||  
 Db 6 YVHDAPV 12

RESULT 45

AAG73128  
 ID AAG73128 standard; peptide; 18 AA.

```

XX AAG73128;
XX AC
XX XX
XX DT 14-AUG-2001 (first entry)
XX XX
XX DE Protease binding site #62.
XX XX
XX KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
XX KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
XX KW haemophilia.
XX XX
XX OS Synthetic.
XX XX
XX FT Key Location/Qualifiers
XX FT Modified-site 3 /label= Aib
XX FT FT /note= "2-aminoisobutyric acid"
XX XX
XX PN W0200118238-Al.
XX XX
XX PD 15-MAR-2001.
XX XX
XX PP 11-SEP-2000; 2000WO-US024882.
XX XX
XX PR 10-SEP-1999; 99US-00394019.
XX XX
XX PA (ONCO-) ONCOIMMUNIN INC.
XX XX
XX PI Komoriya A, Packard BS;
XX XX
XX DR WPI; 2001-389573/41.
XX XX
XX PS New fluorogenic compositions whose fluorescence level increases in the
XX PT presence of active proteases, useful for detecting and localizing
XX PT protease activity in biological samples, particularly in frozen tissue
XX PT samples.
XX XX
XX PS Disclosure; Page 24; 86pp; English.
XX XX
XX CC The present invention describes fluorogenic compositions which can be
XX CC used for the detection of protease activity. This can be useful as an
XX CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,
XX CC thrombosis and arthritis. The fluorogenic compositions comprise a
XX CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The
XX CC peptide is cleaved by a protease and the fluorophores can then be
XX CC detected. The present sequence is one of the peptides described in the
XX CC exemplification of the invention
XX XX
XX SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAVP 7
Db 6 YVHDAVP 12
|||||
|||||

RESULT 46
AAG73127
ID AAG73127 standard; peptide; 18 AA.
XX AC AAG73127;
XX XX
XX DT 14-AUG-2001 (first entry)
XX XX
XX DE Protease binding site #61.
XX XX
XX KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;
XX KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
XX KW haemophilia.
XX XX

```



CC protease activity is detected by fluorescence microscopy, fluorescence  
CC microplate reader, absorption microscopy or confocal fluorescent microplate  
CC fluorimetry, absorption spectroscopy or confocal fluorescent microplate  
CC reader. (I) is useful for delivering a molecule into a cell, and for  
CC screening a test agent for the ability to modulate the activity of the  
CC protease. (I) is useful for detection and localisation of protease  
CC activity in biological samples. (I) also acts as a protease inhibitor,  
CC thus useful as protease inhibitors. (I) enables detection of the protease  
CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
CC represents a fluorogenic protease indicator peptide of the invention.  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
| | | | |  
Db 6 YVHDAVP 12

RESULT 50  
ADN88524  
ID ADN88524 standard; peptide; 18 AA.

XX AC ADN88524;  
XX 12-AUG-2004 (first entry)  
XX DE Fluorogenic protease indicator peptide #220.  
XX KW fluorogenic; protease detection; protease inhibitor.

XX OS Synthetic.  
XX PN US2004096926-A1.  
XX PD 20-MAY-2004.

XX PF 04-JUN-2001; 2001US-00874350.  
XX PR 20-FEB-1997; 97US-00802981.  
XX PR 20-FEB-1998; 98WO-US003000.  
XX PR 10-SEP-1999; 99US-00394019.  
XX PR 11-SEP-2000; 2000WO-US024882.

XX PA (ONCO-) ONCOIMMUNIN INC.  
XX PI Packard BS, Komoriya A;

XX WPI; 2004-399235/37.

XX PT Fluorogenic composition useful for detecting protease activity and test  
XX substance modulating protease activity.

XX PS Disclosure; SEQ ID NO 220; 114pp; English.

XX CC The invention relates to a fluorogenic composition (I) for detecting the  
XX activity of a protease. (I) is useful for detecting the activity of a  
XX protease, which involves contacting the protease with (I), where the  
XX activity of protease is detected in a histological section, cell culture  
XX or tissue section. The cell suspension is derived from the biological  
XX sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
XX protease activity is detected by fluorescence microscopy, fluorescence  
XX microplate reader, absorption microscopy or confocal fluorescent microplate  
XX reader. (I) is useful for delivering a molecule into a cell, and for  
XX screening a test agent for the ability to modulate the activity of the  
XX protease. (I) is useful for detection and localisation of protease  
XX activity in biological samples. (I) also acts as a protease inhibitor,  
XX thus useful as protease inhibitors. (I) enables detection of the protease

CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
CC represents a fluorogenic protease indicator peptide of the invention.  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
| | | | |  
Db 6 YVHDAVP 12

RESULT 51  
ADN88475  
ID ADN88475 standard; peptide; 18 AA.

XX AC ADN88475;  
XX 12-AUG-2004 (first entry)  
XX DE Fluorogenic protease indicator peptide #171.  
XX KW fluorogenic; protease detection; protease inhibitor.

XX OS Synthetic.

XX PN US2004096926-A1.

XX PD 20-MAY-2004.

XX PF 04-JUN-2001; 2001US-00874350.

XX PR 20-FEB-1997; 97US-00802981.  
XX PR 20-FEB-1998; 98WO-US003000.  
XX PR 10-SEP-1999; 99US-00394019.  
XX PR 11-SEP-2000; 2000WO-US024882.

XX PA (ONCO-) ONCOIMMUNIN INC.

XX PI Packard BS, Komoriya A;

XX WPI; 2004-399235/37.

XX PT Fluorogenic composition useful for detecting protease activity and test  
XX substance modulating protease activity.

XX PS Disclosure; SEQ ID NO 171; 114pp; English.

XX CC The invention relates to a fluorogenic composition (I) for detecting the  
XX activity of a protease. (I) is useful for detecting the activity of a  
XX protease, which involves contacting the protease with (I), where the  
XX activity of protease is detected in a histological section, cell culture  
XX or tissue section. The cell suspension is derived from the biological  
XX sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
XX protease activity is detected by fluorescence microscopy, fluorescence  
XX microplate reader, absorption microscopy or confocal fluorescent microplate  
XX reader. (I) is useful for delivering a molecule into a cell, and for  
XX screening a test agent for the ability to modulate the activity of the  
XX protease. (I) is useful for detection and localisation of protease  
XX activity in biological samples. (I) also acts as a protease inhibitor,  
XX thus useful as protease inhibitors. (I) enables detection of the protease  
XX activity, and provides a high intensity fluorescent signal at a visible  
XX wavelength when they are digested by a protease. The present sequence  
XX represents a fluorogenic protease indicator peptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 6 YVHDAPV 12

RESULT 52  
ADN88516  
ID ADN88516 standard; peptide; 18 AA.  
XX  
AC ADN88516;  
XX  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Fluorogenic protease indicator peptide #212.  
XX  
KW fluorogenic; protease detection; protease inhibitor.  
XX  
OS Synthetic.  
XX  
PN US2004096926-A1.  
XX  
PD 20-MAY-2004.  
XX  
PF 04-JUN-2001; 2001US-00874350.  
XX  
PR 20-FEB-1997; 97US-00802981.  
PR 20-FEB-1998; 98WO-US003000.  
PR 10-SEP-1999; 99US-00394019.  
PR 11-SEP-2000; 2000WO-US024882.  
XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX  
PI Packard BS, Komoriya A;  
XX  
DR WPI; 2004-399235/37.  
XX  
PT Fluorogenic composition useful for detecting protease activity and test  
PT substance modulating protease activity.  
XX  
PS Claim 21; SEQ ID NO 212; 114pp; English.  
XX  
CC The invention relates to a fluorogenic composition (I) for detecting the  
CC activity of a protease. (I) is useful for detecting the activity of a  
CC protease, which involves contacting the protease with (I), where the  
CC activity of protease is detected in a histological section, cell culture  
CC or tissue section. The cell suspension is derived from the biological  
CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
CC protease activity is detected by fluorescence microscopy, flow cytometry,  
CC microplate reader, absorption spectroscopy or confocal fluorescent microplate  
CC reader. (I) is useful for delivering a molecule into a cell, and for  
CC screening a test agent for the ability to modulate the activity of the  
CC protease. (I) is useful for detection and localisation of protease  
CC activity in biological samples. (I) also acts as a protease inhibitor,  
CC thus useful as protease inhibitors. (I) enables detection of the protease  
CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
CC represents a fluorogenic protease indicator peptide of the invention.  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 6 YVHDAPV 12

RESULT 53  
ADN88516  
ID ADN88516 standard; peptide; 18 AA.  
XX  
AC ADN88516;  
XX  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Fluorogenic protease indicator peptide #212.  
XX  
KW fluorogenic; protease detection; protease inhibitor.  
XX  
OS Synthetic.  
XX  
PN US2004096926-A1.  
XX  
PD 20-MAY-2004.  
XX  
PF 04-JUN-2001; 2001US-00874350.  
XX  
PR 20-FEB-1997; 97US-00802981.  
PR 20-FEB-1998; 98WO-US003000.  
PR 10-SEP-1999; 99US-00394019.  
PR 11-SEP-2000; 2000WO-US024882.  
XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX  
PI Packard BS, Komoriya A;  
XX  
DR WPI; 2004-399235/37.  
XX  
PT Fluorogenic composition useful for detecting protease activity and test  
PT substance modulating protease activity.  
XX  
PS Claim 21; SEQ ID NO 212; 114pp; English.  
XX  
CC The invention relates to a fluorogenic composition (I) for detecting the  
CC activity of a protease. (I) is useful for detecting the activity of a  
CC protease, which involves contacting the protease with (I), where the  
CC activity of protease is detected in a histological section, cell culture  
CC or tissue section. The cell suspension is derived from the biological  
CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
CC protease activity is detected by fluorescence microscopy, flow cytometry,  
CC microplate reader, absorption spectroscopy or confocal fluorescent microplate  
CC reader. (I) is useful for delivering a molecule into a cell, and for  
CC screening a test agent for the ability to modulate the activity of the  
CC protease. (I) is useful for detection and localisation of protease  
CC activity in biological samples. (I) also acts as a protease inhibitor,  
CC thus useful as protease inhibitors. (I) enables detection of the protease  
CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
CC represents a fluorogenic protease indicator peptide of the invention.  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 6 YVHDAPV 12

RESULT 54  
AAP61520  
ID AAP61520 standard; protein; 193 AA.  
XX  
AC AAP61520;  
XX  
XX 25-MAR-2003 (revised)  
DT 03-OCT-2002 (revised)  
DT 08-AUG-1991 (first entry)

ADN88525  
ID ADN88525 standard; peptide; 18 AA.  
XX  
AC ADN88525;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Fluorogenic protease indicator peptide #221.  
XX  
KW fluorogenic; protease detection; protease inhibitor.  
XX  
OS Synthetic.  
XX  
PN US2004096926-A1.  
XX  
PD 20-MAY-2004.  
XX  
PF 04-JUN-2001; 2001US-00874350.  
XX  
PR 20-FEB-1997; 97US-00802981.  
PR 20-FEB-1998; 98WO-US003000.  
PR 10-SEP-1999; 99US-00394019.  
PR 11-SEP-2000; 2000WO-US024882.  
XX  
PA (ONCO-) ONCOIMMUNIN INC.  
XX  
PI Packard BS, Komoriya A;  
XX  
DR WPI; 2004-399235/37.  
XX  
PT Fluorogenic composition useful for detecting protease activity and test  
PT substance modulating protease activity.  
XX  
PS Disclosure; SEQ ID NO 221; 114pp; English.  
XX  
CC The invention relates to a fluorogenic composition (I) for detecting the  
CC activity of a protease. (I) is useful for detecting the activity of a  
CC protease, which involves contacting the protease with (I), where the  
CC activity of protease is detected in a histological section, cell culture  
CC or tissue section. The cell suspension is derived from the biological  
CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
CC protease activity is detected by fluorescence microscopy, flow cytometry,  
CC microplate reader, absorption spectroscopy or confocal fluorescent microplate  
CC reader. (I) is useful for delivering a molecule into a cell, and for  
CC screening a test agent for the ability to modulate the activity of the  
CC protease. (I) is useful for detection and localisation of protease  
CC activity in biological samples. (I) also acts as a protease inhibitor,  
CC thus useful as protease inhibitors. (I) enables detection of the protease  
CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
CC represents a fluorogenic protease indicator peptide of the invention.  
XX  
SQ Sequence 18 AA;

Query Match 100.0%; Score 40; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.32; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 6 YVHDAPV 12

RESULT 54  
AAP61520  
ID AAP61520 standard; protein; 193 AA.  
XX  
AC AAP61520;  
XX  
XX 25-MAR-2003 (revised)  
DT 03-OCT-2002 (revised)  
DT 08-AUG-1991 (first entry)

```

XX DE Sequence of new antitumour substance designated GIF II.
XX KW Anticancer agent; antitumour.
XX OS Homo sapiens.
XX PN EP187991-A.
XX PD 23-JUL-1986.
XX PF 20-DEC-1985; 85EP-00116344.
XX PR 21-DEC-1984; 84JP-00271207.
XX PR 24-JUN-1985; 85JP-00138280.
XX PR 03-OCT-1985; 85JP-00138281.
XX PR 16-DEC-1985; 85JP-00220882.
XX PA (SAKA ) OTSUKA PHARM CO LTD.
XX PI Nakai S, Kaneta M, Kikumoto Y, Hong YM, Kawai K, Takegata S;
XX PI Ishii K, Yanagihara Y;
XX PS WPI; 1986-190872/30.
XX PR N-PSDB; AAN60285.
XX CC New antitumour substance comprising poly;peptide - useful for specific
XX PT inhibition of growth of tumour cells in humans and animals with low
XX PT toxicity.
XX PS Disclosure; Page 5-6; 112pp; English.
XX CC GIF substances specifically inhibit the growth of tumour cells in humans
XX CC and animals, and so are useful for remission intensifying therapy and
XX CC maintaining therapy. They have very low toxicity. Dose is 0.1-100 mg/kg
XX CC daily. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-
XX CC MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
XX CC field.)
XX SQ Sequence 193 AA;
XX Query Match 100.0%; Score 40; DB 1; Length 193;
XX Best Local Similarity 100.0%; Pred. No. 4;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 37 YVHDAVP 43

RESULT 55
AAP61521
ID AAP61521 standard; protein; 199 AA.
XX AC AAP61521;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 03-OCT-2002 (revised)
XX DT 08-AUG-1991 (first entry)
XX DE Sequence of new antitumour substance designated GIF III.
XX KW Anticancer agent; antitumour.
XX OS Homo sapiens.
XX PN EP187991-A.
XX PD 23-JUL-1986.
XX PF 20-DEC-1985; 85EP-00116344.
XX PR 21-DEC-1984; 84JP-00271207.
XX PR 24-JUN-1985; 85JP-00138280.
XX PR 03-OCT-1985; 85JP-00138281.
XX PR 16-DEC-1985; 85JP-00220882.
XX PA (SAKA ) OTSUKA PHARM CO LTD.
XX PI Nakai S, Kaneta M, Kikumoto Y, Hong YM, Kawai K, Takegata S;
XX PI Ishii K, Yanagihara Y;
XX PS WPI; 1986-190872/30.
XX PR N-PSDB; AAN60285.
XX CC New antitumour substance comprising poly;peptide - useful for specific
XX PT inhibition of growth of tumour cells in humans and animals with low
XX PT toxicity.
XX PS Claim 1; Page 5-6; 112pp; English.
XX CC GIF substances specifically inhibit the growth of tumour cells in humans
XX CC and animals, and so are useful for remission intensifying therapy and
XX CC maintaining therapy. They have very low toxicity. Dose is 0.1-100 mg/kg
XX CC daily. (Updated on 03-OCT-2002 to add missing OS field.) (Updated on 25-
XX CC MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
XX CC field.)
XX SQ Sequence 199 AA;
XX Query Match 100.0%; Score 40; DB 1; Length 199;
XX Best Local Similarity 100.0%; Pred. No. 4.1;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 43 YVHDAVP 49

RESULT 56
AAR52020
ID AAR52020 standard; protein; 202 AA.
XX AC AAR52020;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 19-MAY-1994 (first entry)
XX DE Truncated human Interleukin-1 (amino acids 9-210).
XX KW hIL-1; interleukin; cytokine; truncated; N-terminal deletion;
XX KW C-terminal deletion.
XX OS Homo sapiens.
XX PN EP569687-A1.
XX PD 18-NOV-1993.
XX PF 07-MAY-1985; 93EP-00104177.
XX PR 18-MAY-1984; 84US-00611669.
XX PR 11-FEB-1985; 85US-00700374.
XX PR 07-MAY-1985; 85EP-00303234.
XX PA (NEWB-) NEW ENGLAND MED CENT HOSPITALS.
XX PA (TUFT ) TUFTS COLLEGE.
XX PA (WELL-) WELLESLEY COLLEGE.
XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PI Auron PE, Webb AC, Gehrke L, Dinarello CA, Rosenwasser LJ;
XX PI Rich A, Wolff SM;
XX DR WPI; 1993-360975/46.

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CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 238 AA;

Query Match      100.0%; Score 40; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 82 YVHDAVP 88

RESULT 59
AAR42447
ID AAR42447 standard; protein; 238 AA.
XX
AC AAR42447;
XX
DT 25-MAR-2003 (revised)
DT 12-MAY-1994 (first entry)
XX
DE Human interleukin-1 beta precursor.
XX
KW IL-1beta; colony stimulating factor; CSF; tumour cell growth; inhibition;
KW lymphocyte activating factor; LAF; immunostimulant; anti-inflammatory;
KW immune system; vaccine; cytokine; probe.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 86..238
FT /label= IL-1beta
FT /note= "mature protein"
XX
EP569042-A1.
XX
PN 10-NOV-1993.
XX
PD
XX
PF 12-MAR-1987; 93EP-00107660.
XX
PR 14-MAR-1986; 86JP-00057885.
PR 20-JUN-1986; 86JP-00145830.
PR 09-JUL-1986; 86JP-00161184.
PR 27-AUG-1986; 86JP-00200324.
PR 12-MAR-1987; 87EP-00103609.
XX
PA (SAKA ) OTSUKA PHARM CO LTD.
XX
PI Nakai S, Kaneta M, Kikumoto Y, Hong Y, Kawai K, Takegata S;
PI Ishii K, Yanegihara Y, Hirai Y;
XX
DR WPI; 1993-353161/45.
DR N-PSDB; AAQ51110.
XX
PT Medical use of interleukin-1 beta - for stimulating immunity, promoting
PT colony stimulating factor prodn. and curing inflammation.
XX
PS Example 1); Page 11-14; 31pp; English.
XX
CC Novel uses of interleukin-1 beta are claimed. These include promoting
CC antibody production, promoting production of cytokines such as CSF, IFN,
CC IL-2 and IL-3, as an antitumour agent, as an anti-inflammatory agent and
CC for preventing radiation sickness. A probe was designed having a sequence
CC complementary to the sequence coding for the first 20 N-terminal amino
CC acids of IL-1beta. The probe was used to screen a human lymphocyte cDNA
CC library to select a transformat contg. the IL-1-beta precursor coding
CC sequence. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-
CC MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 238 AA;

Query Match      100.0%; Score 40; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 82 YVHDAVP 88

RESULT 60
AAP50043
ID AAP50043 standard; protein; 269 AA.
XX
AC AAP50043;
XX
DT 25-MAR-2003 (revised)
DT 09-SEP-1991 (first entry)
XX
DE Sequence of interleukin-1 (IL-1).
XX
KW Immunological reagent; T cell stimulant; B cell; immunoglobulin.
XX
OS Homo sapiens.
XX
PN EP161901-A.
XX
PD 21-NOV-1985.
XX
PF 07-MAY-1985; 85EP-00303234.
XX
PR 18-MAY-1984; 84US-00611669.
PR 18-MAY-1984; 84US-00611699.
PR 11-FEB-1985; 85US-00700374.
XX
PA (NEWE-) NEW ENGLAND MEDICAL CENT INC.
PA (TUFT ) TUFTS COLLEGE.
PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PA (WELL-) WELLESLEY COLLEGE.
XX
PI Webb AC, Gehrke L, Dinarello CA, Rosenwasse LJ, Rich A, Wolff SM;
XX
DR WPI; 1985-291135/47.
DR N-PSDB; AAN50060.
XX
PT Recombinant cloning vehicle contg. human interleukin-7 gene - or its
PT fragments, producing new biologically active polypeptide(s).
XX
PS Claim 20; Page 31; 39pp; English.
XX
CC A pure cDNA of 1507 bp (AAN50060) (and its 1-606, 1-677, 1355-1507; 482-
CC 1501; 482-677; and 1355-1507 fragments) are claimed. Also claimed is a
CC recombinant DNA cloning vehicle contg. the human IL-1 gene sequence.
CC Specifically the vehicle contains the sequence coding for the new 287 AA
CC sequence (AAP50043) or the following new fragments (1) 9-224; (2) 1-210-X
CC ; (3) 144-287; and (4) 144-210-(X); (X= Asn-Ser-Ile-Trp-Thr-Gly-Val-Leu-
CC Ser-Leu-Asn-Gln-Val-Leu). (Updated on 25-MAR-2003 to correct PD field.)
CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 269 AA;

Query Match      100.0%; Score 40; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 113 YVHDAVP 119

RESULT 61
AAP81197
ID AAP81197 standard; protein; 269 AA.

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XX AAP81197;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 22-NOV-1990 (first entry)  
 XX  
 DE Interleukin-1 of human peripheral blood macrophage.  
 XX  
 KW non-pyrogenic interleukin-1-like polypeptide; anticancer agent;  
 KW antinfection agent; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP267629-A.  
 XX  
 PD 18-MAY-1988.  
 XX  
 PF 13-NOV-1987; 87EP-00116824.  
 XX  
 PR 14-NOV-1986; 86JP-00271605.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 PI Matsumoto T, Harada N, Yamaguchi K, Komatsu Y, Itoh S;  
 XX  
 DR WPI; 1988-134493/20.  
 DR N-PSDB; AAN82421.  
 XX  
 PT New polypeptide(s) having interleukin-1 activity, free of pyrogenicity -  
 PT obtd. by treating interleukin-1 with Achromobacter protease I or S aureus  
 PT V8 protease.  
 XX  
 PS Disclosure; Page ?; 18pp; English.  
 XX  
 CC This protein is encoded by a sequence obtained after cloning a human  
 CC peripheral blood macrophage-derived cDNA in E.coli The amino acid  
 CC sequence is in agreement with that reported by Auron et al (1984) for IL-  
 CC 1 from equivalent source tissue. An IL-1 expression plasmid based upon  
 CC the cDNA was constructed and used to transform E.coli . The IL-1 produced  
 CC by the transformants was highly purified and enzymatically degraded. The  
 CC polypeptides produced as a result of this treatment were found to have IL  
 CC -1 activity. See also AAP81198-P81202. (Updated on 25-MAR-2003 to correct  
 CC PA field.)  
 XX  
 SQ Sequence 269 AA;  
 Query Match 100.0%; Score 40; DB 1; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 Db 113 YVHDAPV 119  
 |||||  
 RESULT 62  
 AAR15747  
 ID AAR15747 standard; protein; 269 AA.  
 XX  
 AC AAR15747;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-MAR-2003 (revised)  
 DT 27-FEB-1992 (first entry)  
 XX  
 DE Interleukin-1 beta with 116 amino acids added to N-terminus.  
 XX  
 KW IL-1-beta; interleukin 6 inducer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1. .116

FT Region 117. .269  
 FT /label= IL-1\_beta  
 XX  
 PN JP03197433-A.  
 XX  
 PD 28-AUG-1991.  
 XX  
 PF 26-DEC-1989; 89JP-00338998.  
 XX  
 PR 26-DEC-1989; 89JP-00338998.  
 XX  
 PA (SAKA ) OTSUKA PHARM CO LTD.  
 XX  
 DR WPI; 1991-356562/49.  
 XX  
 PD IL-6 production inducer - is deriv. of modified amino acid sequence obtd.  
 PD by modification of interleukin I alpha.  
 PT  
 PS Claim 1; Page 2; 17pp; Japanese.  
 XX  
 CC This peptide is a preferred example of an IL-1 beta derivative with IL-6  
 CC inducing activity. The 116 N-terminal amino acids may also be bonded to  
 CC the C-terminal of IL-1 beta. See also AAR15748. (Updated on 10-MAR-2003  
 CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 269 AA;  
 Query Match 100.0%; Score 40; DB 2; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 Db 113 YVHDAPV 119  
 |||||  
 RESULT 63  
 AAR42213  
 ID AAR42213 standard; protein; 269 AA.  
 XX  
 AC AAR42213;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 19-MAY-1994 (first entry)  
 XX  
 DE Human Interleukin-1.  
 XX  
 KW hIL-1; interleukin; cytokine; truncated; N-terminal deletion;  
 KW C-terminal deletion.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 123. .125  
 FT /label= N-glycosylation\_site  
 FT  
 PN EP569687-A1.  
 XX  
 PD 18-NOV-1993.  
 XX  
 PF 07-MAY-1985; 93EP-00104177.  
 XX  
 PR 18-MAY-1984; 84US-00611669.  
 PR 11-FEB-1985; 85US-00700374.  
 PR 07-MAY-1985; 85EP-00303234.  
 XX  
 PA (NEWB-) NEW ENGLAND MED CENT HOSPITALS.  
 PA (TUFT ) TUFTS COLLEGE.  
 PA (WELL-) WELLESLEY COLLEGE.  
 PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.  
 XX  
 PI Auron PE, Webb AC, Gehrke L, Dinarello CA, Rosenwasser LJ;  
 PI Rich A, Wolff SM;

XX WPI; 1993-360975/46.  
 DR N-PSDB; AAQ50981.  
 XX  
 PT New DNA encoding protein with IL-1 activity - useful in monitoring  
 PT disease states e.g. cancer and studying inflammation e.g. in arthritis  
 PT etc.  
 XX  
 PS Claim 1; Page 11-16; 24pp; English.  
 XX  
 CC DNA comprising part of the nucleotide sequence AAQ50981 which encodes a  
 CC polypeptide having IL-1 activity and a mol.wt. of 20000 is claimed.  
 CC Specifically, the region between nucleotides 111-717 has been found to  
 CC retain hIL-1 activity (see AAQ45464). (Updated on 25-MAR-2003 to correct  
 CC FN field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-  
 CC MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 XX  
 SQ Sequence 269 AA;  
 Query Match 100.0%; Score 40; DB 2; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 DB 113 YVHDAPV 119  
 RESULT 64  
 AAW31668  
 ID AAW31668 standard; protein; 269 AA.  
 XX  
 AC AAW31668;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE Precursor form of leaderless protein IL-1 beta.  
 XX  
 KW Leaderless protein; IL-1 beta; FGF; inhibitor; cardiac glycoside;  
 KW aglycone; treatment; carcinoma; diabetes.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 1..269  
 FT /note= "precursor form of IL-1 beta"  
 FT Protein 117..269  
 FT /note= "the mature form of IL-1 beta starts at the  
 FT position 117"  
 XX  
 PN W09728808-A1.  
 XX  
 PD 14-AUG-1997.  
 XX  
 PF 12-FEB-1997; 97WO-US002237.  
 XX  
 PR 12-FEB-1996; 96US-00599895.  
 XX  
 PA (SCRI ) SCRIPPS RES INST.  
 XX  
 PI Florikiewicz RZ;  
 XX  
 DR WPI; 1997-415065/38.  
 DR N-PSDB; AAV02214.  
 XX  
 PT Inhibition of export of leaderless protein from cells - using cardiac  
 PT glycoside or its aglycone, e.g. ouabain or digoxin.  
 XX  
 PS Disclosure; Page 33-34; 61pp; English.  
 XX  
 CC This is the precursor form of the leaderless protein IL-1 beta. The  
 CC export of such leaderless proteins from a cell can be inhibited by a

CC method which comprises contacting the cell with a cardiac glycoside or  
 CC with an aglycone derivative of a cardiac glycoside. Preferably the  
 CC glycoside is digoxin, strophanthin K, digitoxin, lanatoside A, ouabain,  
 CC oleandrin or acovenoside A, and the aglycone is strophanthidin,  
 CC digoxigenin, digitoxigenin or uzarigenin. The method is useful for  
 CC inhibiting export of leaderless proteins like FGF-1, FGF-2, IL-1 alpha,  
 CC IL-1 beta, PD-ECGF, CNTF, thymosin, parathyrosin, factor XIIIa, vas  
 CC deferens protein, sciatic nerve growth promoting protein, L-14 lectin,  
 CC transglutaminase, thioredoxin-like protein, HIV tat and int-2. Inhibition  
 CC of export of FGF is useful for treating FGF-mediated pathophysiological  
 CC conditions (e.g. melanoma, ovarian carcinoma, teratocarcinoma and  
 CC neuroblastoma). It is useful for inhibiting proliferation of cells  
 CC bearing an FGF-receptor; and for treating complications of diabetes  
 XX  
 SQ Sequence 269 AA;  
 Query Match 100.0%; Score 40; DB 2; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 DB 113 YVHDAPV 119  
 RESULT 65  
 AAW71382  
 ID AAW71382 standard; protein; 269 AA.  
 XX  
 AC AAW71382;  
 XX  
 DT 04-DEC-1998 (first entry)  
 XX  
 DE Interleukin-lbata precursor.  
 XX  
 KW Interleukin-lbata; leaderless protein; inhibition; export; angiogenesis;  
 KW restenosis; treatment; tumour; inflammation; cell proliferation;  
 KW diabetes; retinopathy; infection; polycystic kidney disease;  
 KW atherosclerosis.  
 XX  
 OS Unidentified.  
 XX  
 PN W09837880-A1.  
 XX  
 PD 03-SEP-1998.  
 XX  
 PF 25-FEB-1998; 98WO-US003689.  
 XX  
 PR 26-FEB-1997; 97US-00807014.  
 XX  
 PA (CIBL-) CIBLEX CORP.  
 XX  
 PI Florikiewicz RZ, Baird A;  
 XX  
 DR WPI; 1998-495377/42.  
 DR N-PSDB; AAV60342.  
 XX  
 XX Inhibiting export of leaderless protein with agent that inhibits binding  
 PT to transporter protein - especially for treating angiogenesis and  
 PT restenosis by preventing export of fibroblast growth factor, also methods  
 PT for identifying leaderless proteins and their transporters.  
 XX  
 PS Claim 2; Page 64-65; 116pp; English.  
 XX  
 CC The present sequence represents interleukin-lbata, a leaderless protein.  
 CC A leaderless protein refers to a protein that is found in an  
 CC extracellular environment, but lacks a canonical leader sequence. The  
 CC specification describes a method for inhibiting export of a leaderless  
 CC protein from a cell. The method comprises treating the cell with an agent  
 CC that inhibits binding between the leaderless protein and a transport  
 CC molecule. Treatment with the inhibiting agent is specifically used to  
 CC treat angiogenesis and restenosis, i.e. where expression of FGF-2 is  
 CC inhibited, and the agent is applied to endothelial or smooth muscle

CC cells. Other applications are treatment of tumours (melanoma,  
 CC teratocarcinoma, ovarian carcinoma, bladder cancer and neuroblastoma),  
 CC inflammation, cell proliferation, complications of diabetes (e.g.  
 CC retinopathy), viral, bacterial or fungal infections, polycystic kidney  
 CC disease and atherosclerosis  
 XX  
 SQ Sequence 269 AA;

Query Match 100.0%; Score 40; DB 2; Length 269;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7

|||||

Db 113 YVHDAPV 119

RESULT 66

AA08322

ID AAY08322 standard; protein; 269 AA.

XX AC

XX AAY08322;

XX 16-JUL-1999 (first entry)

XX Human IL-1beta protein.

DE IL-1beta; interleukin-1; human; immunomodulator; immune response; matrix;

XX antigen; immunogen; vaccine; antigen presenting cell.

XX Homo sapiens.

XX W09922763-A2.

XX 14-MAY-1999.

XX 02-NOV-1998; 98WO-US023313.

XX 31-OCT-1997; 97US-00962407.

XX (CIST-) CISTRON BIOTECHNOLOGY INC.

XX Dondero RS, Galton BC, Casey LS;

XX WPI; 1999-313178/26.

XX Composition containing immunomodulator encapsulated in matrix, useful as

XX adjuvant for vaccine.

XX Claim 5; Page 17-18; 18pp; English.

XX This invention describes a novel composition for modulating an immune

XX response in an animal or human which comprises an immunomodulator

XX encapsulated in a matrix. The composition is used to modulate the immune

XX response to an antigen, immunogen or vaccine. Immunomodulators increase

XX the immune response to vaccines etc. Incorporation in a matrix minimizes

XX systemic exposure to the immunomodulator while allowing continuous or

XX controlled delivery of the immunomodulator to antigen presenting cells.

XX This sequence represents the human interleukin-1beta protein which is

XX used in the method of the invention

XX SQ Sequence 269 AA;

Query Match 100.0%; Score 40; DB 2; Length 269;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7

|||||

Db 113 YVHDAPV 119

RESULT 67

AA069531

ID AAY69531 standard; protein; 269 AA.

XX AC

XX AAY69531;

XX 10-APR-2000 (first entry)

XX Human interleukin 1-beta (IL-1-beta) precursor.

DE IL-1-beta precursor; interleukin 1-beta; IL-2 induction;

XX T-cell proliferation; B-cell; immunoglobulin synthesis; adjuvant;

XX immunostimulatory.

XX Homo sapiens.

XX Key

XX Peptide

XX Location/Qualifiers

XX 1..8

XX /note= "Signal peptide"

XX Cleavage-site

XX 8..9

XX Protein

XX 9..210

XX /note= "Mature human IL-1-beta"

XX Cleavage-site

XX 210..211

XX Peptide

XX 211..269

XX US5998578-A.

XX 07-DEC-1999.

XX 07-JUN-1995;

XX 95US-00474829.

XX 18-MAY-1984;

XX 84US-00611669.

XX 08-JAN-1987;

XX 87US-00004319.

XX 25-APR-1988;

XX 88US-00185731.

XX 30-AUG-1990;

XX 90US-00557279.

XX 06-MAY-1992;

XX 92US-00880476.

XX 01-JUN-1993;

XX 93US-00071031.

XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.

XX (TUFT ) TUFTS COLLEGE.

XX (WELL-) WELLESLEY COLLEGE.

XX Dinarello CA, Webb AC, Rich A, Wolff SM, Auron PE;

XX WPI; 2000-104622/09.

XX N-PSDB; AA255973.

XX Purified truncated polypeptide fragment of human interleukin-1beta

XX precursor polypeptide useful in producing antibodies.

XX Claim 2; Fig 2A-B; 11pp; English.

XX This sequence represents a human interleukin 1-beta (IL-1-beta) precursor

XX protein, isolated from monocytes. The invention relates to a purified

XX truncated fragment of human IL-1-beta precursor protein (i.e., not the

XX mature form of IL-1-beta) which has IL-1-beta biological activity as

XX determined by mouse thymocyte assay. IL-1 plays a central role as a

XX mediator of host immunological and defence functions. It can induce the

XX production of IL-2 by activating T-cells (IL-2 stimulates the T-cells to

XX proliferate), and increases B-cell proliferation and immunoglobulin (Ig)

XX synthesis. IL-2 also has inflammatory properties, increasing levels of

XX prostaglandin E2 in a variety of tissues. The truncated IL-1-beta

XX precursor protein is useful in producing antibodies that are

XX immunoreactive with it. Genes encoding the truncated IL-1-beta precursor

XX are useful for detecting related DNA sequences in the human genome,

XX reduced IL-1 production being associated with certain cancers and

XX malnutrition. IL-1, or associated fragments, can be used as an

XX immunological reagent or adjuvant in humans or other animals due to its

XX ability to stimulate T and B-cells and increase Ig synthesis. The

XX truncated IL-1-beta precursor may also be also useful in the production

XX of IL-2, via activation of T-cells

XX SQ Sequence 269 AA;

```
Query Match      100.0%; Score 40; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      113 YVHDAPV 119

RESULT 68
AAB37790
ID AAB37790 standard; protein; 269 AA.
XX
AC AAB37790;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human interleukin-1beta.
XX
KW Human; interleukin-1; IL-1; IL-1alpha; IL-1beta; IL-1 receptor;
KW antiinflammatory; haemostatic; antibacterial; immunosuppressive;
KW immunomodulator; cardiant; cytostatic; neuroprotective; respiratory;
KW inflammation; infection; sepsis; cachexia; autoimmune disorder;
KW cardiovascular disorder; chronic myelogenous leukaemia;
KW multiple sclerosis; inflammatory bowel disease; Crohn's disease.
XX
OS Homo sapiens.
XX
PN WO20064479-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-US011700.
XX
PR 27-APR-1999; 99US-00301274.
XX
PA (ANTI-) ANTIBODY SYSTEMS INC.
XX
PI Fredeking TM, Ignatyev GM;
XX
WPI; 2000-679646/66.
XX
PT Novel compositions comprising tetracycline or tetracycline-like compounds
PT for the treatment and/or prevention of acute inflammatory responses and
PT diseases, e.g. septic shock and immune complex-induced colitis.
XX
PS Disclosure; Page 148-149; 183pp; English.
XX
CC The present sequence is given in a specification relating to novel
CC compositions and methods containing tetracycline or tetracycline-like
CC compounds for treating and/or preventing acute inflammatory responses and
CC diseases. Such diseases include acute inflammatory conditions associated
CC with viral haemorrhagic diseases (including diseases caused by
CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses),
CC Parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
CC disorders, acute cardiovascular events, chronic myelogenous leukaemia and
CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
CC immune complex-induced colitis, cerebrospinal fluid inflammation,
CC multiple sclerosis, inflammatory responses associated with trauma,
CC systemic inflammatory response syndrome (SIRS), adult respiratory
CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
CC and Crohn's disease
XX
SQ Sequence 269 AA;

Query Match      100.0%; Score 40; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      113 YVHDAPV 119

RESULT 70
AAB35251
```

```
RESULT 69
AAY96877
ID AAY96877 standard; protein; 269 AA.
XX
AC AAY96877;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human precursor interleukin 1-beta.
XX
KW IL 1-beta; interleukin 1-beta; precursor; transport molecule; golgi;
KW Leaderless; endoplasmic reticulum; protein export; detection; inhibitor.
XX
OS Homo sapiens.
XX
PN US6083706-A.
XX
PD 04-JUL-2000.
XX
PF 25-FEB-1998; 98US-00030613.
XX
PR 26-FEB-1997; 97US-00807014.
XX
PA (CIBL-) CIBLEX CORP.
XX
PI Baird A, Florkiewicz RZ;
XX
WPI; 2000-464338/40.
XX
N-PSDB; AAA53568.
XX
PT Detecting transport molecules, useful for identifying proteins that
PT mediate leaderless protein export across cell membranes, by contacting
PT cell extracts with a fusion protein of leaderless protein and a tag to
PT form a complex.
XX
PS Disclosure; Col 47-48; 64pp; English.
XX
CC Detecting a transport molecule involved in non-endoplasmic reticulum
CC (ER)/Golgi leaderless protein export, comprises contacting test cell
CC extracts or membranes with a fusion protein of a leaderless protein and a
CC tag to form a complex of the fusion protein bound to the transport
CC molecule, and detecting the transport molecule in an isolated complex.
CC The leaderless protein is a protein found in the extracellular
CC environment that lacks a canonical leader sequence, interleukin (IL) 1-
CC alpha, or 1-beta, fibroblast growth factor (FGF) 1 or 2, human
CC immunodeficiency virus (HIV) tat, platelet-derived endothelial cell
CC growth factor (PD-ECGF), ciliary neurotrophic factor (CNTF), sciatic
CC nerve growth-promoting activity, vas deferens protein, transglutaminase,
CC L-14 lectin, factor XIIIa, thioredoxin-like protein (ADF), thymosin,
CC parathymosin, mammary-derived growth inhibitor, galectin or rhodanase.
CC The method is used to detect proteins, complexes of proteins, or parts of
CC a larger complex, that bind to and mediate the transport of leaderless
CC proteins, e.g. Na+/K+ ATPase which is an integral membrane protein
CC responsible for transporting sodium and potassium ions across the cell
CC membrane using ATP as the driving force. Transport molecules detected by
CC the method are used in assays to identify inhibitors of the interaction
CC with a leaderless protein
XX
SQ Sequence 269 AA;

Query Match      100.0%; Score 40; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      113 YVHDAPV 119

RESULT 70
AAB35251
```

ID AAB35251 standard; protein; 269 AA.  
XX  
AC AAB35251;  
XX  
DT 04-MAY-2001 (first entry)  
XX  
DE Human pre-interleukin-1 beta.  
XX  
KW Human; ICE; interleukin-1 beta converting enzyme; inflammatory disorder;  
KW autoimmune condition; IL-1beta.  
XX  
OS Homo sapiens.  
XX  
PN US6187550-B1.  
XX  
PD 13-FEB-2001.  
XX  
PF 13-NOV-1996; 96US-00748547.  
XX  
PR 27-JUL-1994; 94US-00280889.  
XX  
PA (BADI ) BASF AG.  
XX  
PI Ghayur T, McGuinness LM;  
XX  
XX WPI; 2001-210325/21.  
XX  
DR N-PSDB; AAF24472.  
XX  
XX Identifying genes and compositions that interact with interleukin-1beta  
PT (IL-1 beta) processing pathways comprises using a cell having a first  
PT gene for precursor IL-1beta and a second gene for an IL-1beta converting  
PT enzyme.  
XX  
PS Disclosure; Fig 2; 49pp; English.  
XX  
XX The present invention describes methods of identifying compositions with  
CC activity in the interleukin-1beta (IL-1beta) processing or secretory  
CC pathways, involving applying a test composition to a cell comprising a  
CC gene for IL-1beta and IL-1beta converting enzyme (ICE), and determining  
CC the effect on the cell, where a change indicates that the composition has  
CC such activity. This is useful in the identification of compounds for use  
CC in the treatment of inflammatory disorders and autoimmune conditions. The  
CC present sequence is the human IL-1beta protein  
XX  
SQ Sequence 269 AA;  
Query Match 100.0%; Score 40; DB 4; Length 269;  
Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;  
QY 1 YVHADPV 7  
DB 113 YVHADPV 119  
RESULT 71  
AAB97079  
ID AAB97079 standard; protein; 269 AA.  
XX  
AC AAB97079;  
XX  
XX 02-AUG-2001 (first entry)  
DT  
XX Human IL1B.  
DE  
XX Human; IL1B; interleukin-1 beta; gene therapy; antiinflammatory;  
KW single nucleotide polymorphism; SNP; polymorphic site;  
KW inflammatory disorder; immune disorder.  
XX  
XX Homo sapiens.  
OS  
XX WO200121639-A1.  
PI  
XX

PD 29-MAR-2001.  
XX  
PF 20-SEP-2000; 2000WO-US025794.  
XX  
PR 22-SEP-1999; 99US-0155412P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
XX Chew A, Choi J, Denton RR, Nandabalan K, Stephens JC;  
PI WPI; 2001-389617/41.  
XX  
DR N-PSDB; AAH24369.  
XX  
XX New polynucleotide useful for therapeutic purposes, comprises nucleotide  
PT polymorphisms of interleukin-1B gene.  
XX  
XX Disclosure; Fig 3; 57pp; English.  
XX  
XX The present invention relates to an isolated polynucleotide comprising a  
CC nucleotide sequence which is a polymorphic variant of the fully defined  
CC 7821 base pair interleukin-1 beta (IL1B) gene reference sequence given in  
CC the specification or its fragment or complement. The IL1B gene  
CC polymorphic variant is useful for therapeutic purposes, for studying the  
CC expression and biological function of IL1B, for developing drugs  
CC targeting this protein, and in diagnostics and forensic applications. The  
CC method is useful for developing tests and therapeutic treatments for  
CC inflammatory and immune disorders. The present sequence is the protein  
CC encoded by the IL1B gene reference sequence  
XX  
SQ Sequence 269 AA;  
Query Match 100.0%; Score 40; DB 4; Length 269;  
Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0;  
QY 1 YVHADPV 7  
DB 113 YVHADPV 119  
RESULT 72  
AAU80166  
ID AAU80166 standard; protein; 269 AA.  
XX  
AC AAU80166;  
XX  
XX 15-JUL-2002 (first entry)  
DT  
XX Human interleukin 1 beta.  
DE  
XX Human; SNP; single nucleotide polymorphism; inflammation;  
KW rheumatoid arthritis; postmenopausal osteoporosis; IBS;  
KW inflammatory bowel disease; insulin-dependent diabetes mellitus;  
KW multiple sclerosis; local osteolytic hypercalcaemia; chromosome 2q14;  
KW bone marrow cancer; gastric cancer; hypochlorhydria; periodontitis;  
KW alopecia areata; tuberculosis; diabetic neuropathy; haplotype; genotype;  
KW Epstein-Barr virus infection; Interleukin 1 beta; IL1beta.  
XX  
XX Homo sapiens.  
OS  
XX WO200224951-A1.  
FN  
XX 28-MAR-2002.  
PD  
XX 22-MAY-2001; 2001WO-US016612.  
PF  
XX 20-SEP-2000; 2000WO-US025794.  
PR  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Bentivegna SC, Chew A, Choi JY, Denton RR, Lee HH, Nandabalan K;  
PI Stephens JC;  
PI  
XX

DR WPI: 2002-383198/41.  
DR N-PSDB; ABK50291, ABK50292.  
XX Novel genetic variants of interleukin 1, beta gene useful for screening  
PT drugs to treat diseases e.g. inflammatory and immune disorders.  
XX  
PS Disclosure; Fig 3; 71pp; English.  
XX  
XX The invention relates to an isolated polynucleotide having a sequence  
CC comprising interleukin 1, beta (IL1B) isogene selected from 18 isogenes  
CC with regions of a 7824 base pair sequence, given in specification, and  
CC defined by corresponding set of single nucleotide polymorphisms (SNP) and  
CC its fragment or complementary sequence. Also included are a recombinant  
CC non-human organism transformed or transfected with the IL1B gene, a  
CC computer system for storing and analysing polymorphism data for IL1B  
CC gene, a genome anthology for IL1B gene which comprises IL1B isogenes  
CC defined by any one of haplotypes 1-18 as given in the specification,  
CC haplotyping IL1B gene of an individual comprising determining which of  
CC the 1-18 haplotypes (HTS) defines one copy or both copies of the  
CC individuals IL1B gene, genotyping IL1B of an individual comprising  
CC determining for the two copies of IL1B gene present in the individual,  
CC identifying an association between a trait and at least one HTS or  
CC haplotype pair of the IL1B gene, a composition comprising at least  
CC a genotyping oligonucleotide for detecting a polymorphism in IL1B gene and  
CC oligonucleotides designed to genotype each of PS. The haplotype/genotype  
CC information is useful for diagnosing/predicting susceptibility to such  
CC diseases as inflammation, rheumatoid arthritis, postmenopausal  
CC osteoporosis, IBS, inflammatory bowel disease, insulin-dependent diabetes  
CC mellitus, multiple sclerosis, local osteolytic hypercalcaemia, bone  
CC marrow cancer, gastric cancer, hypochlorhydria, periodontitis, alopecia  
CC areata, tuberculosis, diabetic neuropathy and Epstein-Barr virus  
CC infection. The gene is located on chromosome 2q14. The isogenes and  
CC protein are useful for screening drugs targeting IL1B. The present  
CC sequence is the human IKIL1B protein  
XX  
SQ Sequence 269 AA;  
  
Query Match 100.0%; Score 40; DB 5; Length 269;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YVHDAVP 7  
Db 113 YVHDAVP 119  
|||||  
  
RESULT 73  
AAU11115  
ID AAU11115 standard; protein; 269 AA.  
XX  
XX AAU11115;  
XX  
XX 14-FEB-2002 (first entry)  
XX  
XX Human Interleukin-1beta precursor protein.  
XX  
XX Human; fibroblast growth factor 2; FGF-2; cytostatic; antidiabetic;  
KW cell transport pathway; leaderless protein; FGF-1; interleukin-1;  
KW IL-1alpha; IL-1beta; tumour; melanoma; teratocarcinoma;  
KW ovarian carcinoma; bladder tumour; neuroblastoma; diabetes; angiogenesis;  
KW inflammation; restenosis; viral infection; bacterial infection;  
KW fungal infection; diabetic retinopathy; polycystic kidney disease;  
KW atherosclerosis.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH 1. .116  
FT Peptide /label= Unidentified  
FT /note= "Cleaved to leave the mature IL-1beta protein"  
FT 117. .269  
FT Protein /label= Mature IL-1beta  
FT

XX US6306613-B1.  
XX 23-OCT-2001.  
PD  
XX 01-DEC-1999; 99US-00451905.  
XX  
XX 26-FEB-1997; 97US-00807014.  
XX 25-FEB-1998; 98US-00030613.  
XX (CIBL-) CIBLEX CORP.  
XX  
XX Florkiewicz RZ, Baird A, Warnock DR;  
PI  
XX WPI: 2002-040200/05.  
DR N-PSDB; AAS17405.  
XX  
XX Detecting components of a cell transport pathway, for identifying small  
PT export modulation molecules, comprises contacting cell extracts with a  
PT fusion protein of a transport molecule comprising a trifuunctional protein  
PT beta subunit.  
XX  
XX Example 13; Col 57-59; 80pp; English.  
XX  
XX The invention relates to detecting components of a cell transport  
CC pathway, comprising contacting cell extracts, cell membranes or other  
CC subcellular fractions containing components of a cell transport pathway  
CC with a fusion protein of a transport molecule and a tag, where the  
CC transport molecule comprises a trifuunctional protein beta subunit to form  
CC a complex of the fusion protein with components of the cell transport  
CC pathway. One or more components of the transport pathway are leaderless  
CC proteins e.g. fibroblast growth factor 1 and2 (FGF-1,FGF-2), interleukin-  
CC 1alpha (IL-1alpha) and interleukin-1beta, (IL-1beta). The method is used  
CC for detecting components of a cell transport pathway, useful for  
CC identifying small molecules for export modulation that can be used to  
CC treat various conditions including tumours(e.g. melanoma,  
CC teratocarcinoma, ovarian carcinoma, bladder tumours and neuroblastomas),  
CC diabetes, angiogenesis, inflammation, restenosis, viral infection,  
CC bacterial infection, fungal infection, diabetic retinopathy, polycystic  
CC kidney disease and atherosclerosis. The present sequence represents IL-  
CC 1beta precursor protein, a leaderless protein used to identify candidate  
CC transport molecules using the method of the invention  
XX  
SQ Sequence 269 AA;  
  
Query Match 100.0%; Score 40; DB 5; Length 269;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YVHDAVP 7  
Db 113 YVHDAVP 119  
|||||  
  
RESULT 74  
AAE33564  
ID AAE33564 standard; protein; 269 AA.  
XX  
XX AAE33564;  
XX  
XX 16-APR-2003 (first entry)  
XX  
XX Human interleukin-1B (IL-1B).  
XX  
XX Drug screening; fungicide; gene therapy; antibacterial; infection;  
KW virucide; human; interleukin-1; IL-1.  
XX  
XX Homo sapiens.  
XX  
XX WO2002101015-A2.  
XX  
XX 19-DEC-2002.  
XX

PF 11-JUN-2002; 2002WO-US018346.  
 XX 11-JUN-2001; 2001US-0297305P.  
 XX (INTE-) INTERLEUKIN GENETICS INC.  
 PA Dower S, Duff GW;  
 XX WPI; 2003-148793/14.  
 XX New detection reagent, useful for monitoring molecular assembly events to  
 PT permit the dissection of genetic and non-genetic influences on biological  
 PT activity, comprises an interactive sensor pair.  
 XX Disclosure; Fig 4; 56pp; English.  
 XX The invention relates to methods, compositions and apparatus for  
 CC monitoring molecular assembly events. It also relates to a detection  
 CC reagent comprising an interactive sensor pair. The detection reagent is  
 CC useful for monitoring molecular assembly events to permit the dissection  
 CC of genetic and non-genetic influences on a particular biological  
 CC activity. The method is useful for linking genetic variations to  
 CC molecular and physiological events, drug screening, diagnostics, therapy  
 CC selection and dosing, patient monitoring or environmental safety. The  
 CC interactive sensor pairs may be used to screen for and identify novel  
 CC agonists and antagonists or other molecules that modulate a biological  
 CC activity. The method is also useful for selecting an appropriate targeted  
 CC therapeutic for a subject having an infection, including viral, bacterial  
 CC or fungal infection. It is also used in gene therapy. The present  
 CC sequence is human interleukin-1 (IL-1). This sequence is used to  
 CC illustrate the method of the invention  
 XX  
 SQ Sequence 269 AA;  
 Query Match 100.0%; Score 40; DB 6; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAVP 7  
 Db 113 YVHDAVP 119  
 |||||  
 RESULT 75  
 ABU08119  
 ID ABU08119 standard; protein; 269 AA.  
 XX  
 AC ABU08119;  
 XX  
 DT 10-MAY-2003 (first entry)  
 XX  
 DE Recombinant interleukin 1 beta protein.  
 XX  
 KW Interleukin 1; human; interleukin1; IL-1; IL-1-receptor; IL-1R;  
 KW IL-R accessory protein; IL-Racp; protein-protein interaction.  
 XX  
 OS Homo sapiens.  
 XX GB2375604-A.  
 XX  
 PD 20-NOV-2002.  
 XX  
 PF 18-MAY-2001; 2001GB-00012251.  
 XX  
 PR 18-MAY-2001; 2001GB-00012251.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Bertelli F, Brown JP, Gee NS;  
 XX WPI; 2003-150708/15.  
 DR N-PSDB; ABX12959.  
 XX

PT Determining ability of test compound to modulate formation of interleukin  
 PT soluble trimolecular complex, by bringing into contact the components of  
 PT the complex and test compound and determining amount of complex formed.  
 XX Disclosure; Page 133-134; 171pp; English.  
 XX This invention relates to a novel assay for determining the ability of a  
 CC test compound to modulate the formation of a trimolecular complex (TC)  
 CC including interleukin (IL), a soluble IL-receptor (IL-R) polypeptide and  
 CC a soluble IL-R accessory protein (IL-Racp). The method comprises bringing  
 CC into contact an IL polypeptide, a soluble IL-R polypeptide, a soluble IL-  
 CC Racp polypeptide and a test compound, and determining the amount of TC  
 CC formed. The method of the invention is useful for determining the ability  
 CC of a test compound to modulate the formation of a trimolecular complex  
 CC including IL, a soluble IL-R and a soluble IL-Racp. The method is useful  
 CC for high throughput screening and enables direct measurement of protein  
 CC binding characteristics. It is also useful for identifying small molecule  
 CC inhibitors of TC and hence of IL-1 biological activity. The method may be  
 CC used in screening methods and assays for agents which modulate the  
 CC interaction between IL and IL-R, and/or the interaction between IL-Racp  
 CC and the IL/IL biomolecular complexes. This method identifies small  
 CC molecule inhibitors of TC and hence IL-1 biological activity, and  
 CC provides a significant advantage over prior methods since it is possible  
 CC to dose orally and to reduce the cost of production of such compounds  
 CC compared to the production cost of recombinant proteins. The main  
 CC advantage of using soluble forms of the proteins in the method is the  
 CC ease with which these reagents enable the formatting and running of High  
 CC Throughput Screening (HTS) assays. The present sequence represents an  
 CC interleukin 1 family protein used in the method of the invention  
 XX  
 SQ Sequence 269 AA;  
 Query Match 100.0%; Score 40; DB 6; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAVP 7  
 Db 113 YVHDAVP 119  
 |||||  
 RESULT 76  
 ABO10812  
 ID ABO10812 standard; protein; 269 AA.  
 XX  
 AC ABO10812;  
 XX  
 DT 21-AUG-2003 (first entry)  
 XX  
 DE Human interleukin 1 beta, IL-1beta.  
 XX  
 KW Human; interleukin-1; IL-1 alpha; IL-1 beta; acute pancreatitis; ALS;  
 KW amyotrophic lateral sclerosis; Alzheimer's disease; cachexia; anorexia;  
 KW asthma; pulmonary disease; atherosclerosis; autoimmune vasculitis;  
 KW chronic fatigue syndrome; coronary condition; congestive heart failure;  
 KW cancer; diabetes; endometritis; fever; glomerulonephritis; ARDS;  
 KW graft versus host disease; haemorrhagic shock; inflammatory condition;  
 KW inflammatory bowel disease; osteoarthritis; rheumatoid arthritis;  
 KW ischaemia; stroke; lung disease; adult respiratory distress syndrome;  
 KW multiple sclerosis; pain; Parkinson's disease; psoriasis; septic shock;  
 KW reperfusion injury; sleep disturbance; uveitis; infection.  
 XX  
 OS Homo sapiens.  
 XX US2003026806-A1.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 29-OCT-2001; 2001US-00011931.  
 XX  
 PR 27-OCT-2000; 2000US-0244118P.  
 XX  
 PA (AMGE-) AMGEN INC.

XX	Witte A, Varnum BC, Qian X, Vezina C;
XX	WPI; 2003-479525/45.
DR	
XX	Treating interleukin-1 mediated disease, by administering an IL-1
PT	selective binding agent that binds to IL-alpha or IL-1beta, such that
PT	the complex binds to IL-1 receptor without activating the receptor.
XX	
PS	Claim 8; Page 4; 39pp; English.
XX	
CC	The invention relates to treating interleukin-1 (IL-1)-mediated disease,
CC	or blocking IL-1alpha and IL-1beta from binding to the IL-1 receptor,
CC	involving administering an IL-1 selective binding agent (e.g. a humanised
CC	mouse anti-IL-1 antibody) that is capable of binding to IL-1 alpha or IL-
CC	beta, where the selective binding agent-IL-1 complex is capable of
CC	binding to IL-1 receptor without activating the receptor. The activities
CC	of mouse, chimeric and humanised monoclonal antibody (MAb)201 in
CC	blocking formation of IL-1beta/IL-1 receptor/IL-1kacp complex were
CC	studied. The results showed that anti-IL-beta antibody MAB201 is the
CC	most effective inhibitor of IL-beta signalling. The method is useful for
CC	treating IL-1-mediated disease e.g. acute pancreatitis, amyotrophic
CC	lateral sclerosis (ALS), Alzheimer's disease, cachexia, anorexia, asthma,
CC	pulmonary diseases, atherosclerosis, autoimmune vasculitis, chronic
CC	fatigue syndrome, Clostridium associated illness, coronary conditions
CC	(e.g. congestive heart failure, coronary restenosis, coronary graft),
CC	infarction, myocardial dysfunction and coronary artery bypass graft),
CC	cancers, diabetes, endometriosis, fever, fibromyalgia, hyperalgesia,
CC	glomerulonephritis, graft versus host disease; haemorrhagic shock,
CC	inflammatory bowel disease, inflammatory conditions (e.g. osteoarthritis,
CC	psoriatic arthritis and rheumatoid arthritis), inflammatory eye disease,
CC	ischaemia including cerebral ischaemia, stroke, Kawasaki's disease,
CC	learning impairment, lung diseases (adult respiratory distress syndrome
CC	(ARDS)), multiple sclerosis, myopathies, neurotoxicity, osteoporosis,
CC	pain, Parkinson's disease, periodontal disease, preterm labour,
CC	psoriasis, reperfusion injury, septic shock, side effects from radiation
CC	therapy, temporal mandibular joint disease, sleep disturbance, uveitis
CC	and inflammatory conditions resulting from strain, sprain, cartilage
CC	damage, trauma, orthopaedic surgery and infection. The present sequence
CC	is a human interleukin-1 protein
XX	
XX	Sequence 269 AA;
XX	
Qy	Query Match 100.0%; Score 40; DB 6; Length 269;
	Best Local Similarity 100.0%; Pred. No. 5.7;
Db	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 YVHDAPV 7
Db	113 YVHDAPV 119
RESULT 77	
ADC78855	
ID	ADC78855 standard; protein; 269 AA.
XX	
AC	ADC78855;
XX	
DT	01-JAN-2004 (first entry)
XX	
DE	Human PRO protein #42.
XX	
KW	human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW	Crohn's disease.
XX	
OS	Homo sapiens.
XX	
PN	WO2003034984-A2.
XX	
PD	01-MAY-2003.
XX	
XX	15-OCT-2002; 2002WO-US033070.
XX	



XX Claim 25; SEQ ID NO 91; 424pp; English.

XX This invention relates to novel human genes and gene product which are

XX implicated in certain disease states. Compounds which modulate the

XX proteins of the invention may have cytostatic, antiinflammatory, the

XX ophthalmological, antiarteriosclerotic or vulnary activities. The

XX sequences of the invention may be useful for gene therapy. The invention

XX may be useful for diagnosing or treating a hypoxia-regulated condition,

XX such as tumorigenesis, angiogenesis, apoptosis, inflammation,

XX erythropoiesis, or the biological response to hypoxia conditions

XX including processes such as glycolysis, gluconeogenesis, glucose

XX transport, catecholamine synthesis, iron transport or nitric oxide

XX synthesis. The disease includes cancer, ischaemic conditions, reperfusion

XX injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,

XX inflammatory conditions or wound healing. The present sequence is that of

XX a disease related protein of the invention.

SQ Sequence 269 AA;

Query Match 100.0%; Score 40; DB 7; Length 269;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7

DB 113 YVHDAPV 119

RESULT 79

ADH17054

ID ADH17054 standard; protein; 269 AA.

XX

XX ADH17054;

XX

XX 11-MAR-2004 (first entry)

XX Human interleukin-1 beta protein.

XX

XX tyrosine kinase activity; type 1 plasminogen activator inhibitor; PAI-1;

XX TIMP-1; tissue inhibitor of metalloproteinase 1; vinculin;

XX vascular endothelial growth factor; VEGF; placental growth factor; PLGF;

XX migration inhibitory factor; MIG; human; interleukin-1 beta.

XX

XX Homo sapiens.

XX

XX WO2003097854-A2.

XX

XX 27-NOV-2003.

XX

XX 19-MAY-2003; 2003WO-US015711.

XX

XX 17-MAY-2002; 2002US-0380872P.

XX

XX 24-FEB-2003; 2003US-0448874P.

XX

XX 24-FEB-2003; 2003US-0448922P.

XX

XX (SUGEN-) SUGEN INC.

XX

XX Mcrimoto A, Deprimo S, O'farrell A, Smolich BD, Manning WC;

XX Walter SA, Schilling JW, Cherrington J;

XX WPI; 2004-042604/04.

XX

XX Determining whether a test compound inhibits tyrosine kinase activity in

XX a mammal by exposing the mammal to the test compound and measuring in the

XX mammal the level of at least one of the measured proteins or mRNA

XX transcripts.

XX

XX Disclosure; SEQ ID NO 53; 408pp; English.

XX

XX The invention relates to a novel method for determining whether a test

XX compound inhibits tyrosine kinase activity in a mammal comprising

XX measuring in the mammal the level of at least one of the proteins and/or

CC mRNA transcripts or genes for such proteins comprising type 1 plasminogen

CC activator inhibitor (PAI-1), TIMP-1 (tissue inhibitor of

CC metalloproteinase 1), vinculin, vascular endothelial growth factor

CC (VEGF), placental growth factor (PLGF), VEGF/PLGF heterodimers or

CC migration inhibitory factor (MIG), exposing the mammal to the test

CC compound and then measuring in the mammal the level of at least one of

CC the proteins and/or mRNA transcripts previously measured. The method of

CC the invention may be useful for determining whether a test compound

CC inhibits tyrosine kinase activity in a mammal. The current sequence is

CC that of the tyrosine kinase activity inhibition-related protein of the

XX invention.

XX

SQ Sequence 269 AA;

Query Match 100.0%; Score 40; DB 8; Length 269;

Best Local Similarity 100.0%; Pred. No. 5.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7

DB 113 YVHDAPV 119

RESULT 80

ADN07707

ID ADN07707 standard; protein; 269 AA.

XX

XX ADN07707;

XX

XX 01-JUL-2004 (first entry)

XX Human beta-interleukin-1 protein.

XX

XX Protease; stem cell; bone marrow failure disorder; aplastic anaemia;

XX myeloproliferative disorder; multiple myeloma; gene therapy; human;

XX beta-interleukin.

XX

XX Homo sapiens.

XX

XX US2004071687-A1.

XX

XX 15-APR-2004.

XX

XX 28-MAY-2003; 2003US-00447315.

XX

XX 28-MAY-2002; 2002US-0383658P.

XX

XX (RAFI/) RAFII S.

XX (HEIS/) HEISSIG B.

XX (HATT/) HATTORI K.

XX

XX Rafii S, Heissig B, Hattori K;

XX

XX WPI; 2004-328523/30.

XX

XX N-PSDB; ADN07708.

XX

XX GENBANK; 30583265.

XX

XX Recruiting adult stem cells in an animal for treating aplastic anemia or

XX multiple myeloma by administering a protease or its activator so that the

XX stem cells can proliferate, self-renew, differentiate or mobilize to a

XX target site.

XX

XX Disclosure; SEQ ID NO 13; 77pp; English.

XX

XX The present invention relates to the use of proteases to recruit stem

XX cells from the niches they normally occupy. The invention is useful for

XX recruiting adult stem cells for treating bone marrow failure disorder

XX such as aplastic anaemia and myeloproliferative disorder such as multiple

XX myeloma. The invention is also useful in gene therapy. The present

XX sequence is human beta-interleukin-1 protein.

XX

SQ Sequence 269 AA;

Query Match 100.0%; Score 40; DB 8; Length 269;  
Best Local Similarity 100.0%; Pred. No. 5.7; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
113 YVHDAPV 119

Db

RESULT 81  
ABM80337  
ID ABM80337 standard; protein; 269 AA.  
XX  
AC ABM80337;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Tumour-associated antigenic target (TAT) polypeptide PRO65, SEQ:848.  
XX  
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
KW chromosome identification; chromosome mapping; gene mapping;  
KW gene therapy; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2004030615-A2.  
XX  
PD 15-APR-2004.  
XX  
PF 29-SEP-2003; 2003WO-US028547.  
XX  
PR 02-OCT-2002; 2002US-0414971P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Wu TD, Zhang Z, Zhou Y;  
XX  
DR WPI: 2004-347921/32.  
DR N-PSDB; ACN37754.  
XX  
XX New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a  
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.  
XX  
PS Claim 12; SEQ ID NO 848; 7273pp; English.  
XX  
XX The invention relates to human tumour-associated antigenic target (TAT)  
CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
CC overexpressed in cancer tissues compared to normal tissues, and may thus  
CC serve as effective targets for the diagnosis and treatment of cancer in  
CC mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
CC TAT polypeptide; and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention  
XX  
SQ Sequence 269 AA;

Query Match 100.0%; Score 40; DB 8; Length 269;  
Best Local Similarity 100.0%; Pred. No. 5.7; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
113 YVHDAPV 119

Db

RESULT 82  
ADP54072  
ID ADP54072 standard; protein; 269 AA.  
XX  
AC ADP54072;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human PRO protein sequence SEQ ID NO:48.  
XX  
KW human; PRO; immune related disease; inflammatory immune response;  
KW immune response stimulation; anti-allergic; antianemic; antiarthritic;  
KW antidiabetic; antidiabetic; anti-inflammatory; antipsoriatic;  
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;  
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
KW virucide; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2004039956-A2.  
XX  
PD 13-MAY-2004.  
XX  
PF 28-OCT-2003; 2003WO-US034381.  
XX  
PR 29-OCT-2002; 2002US-0422472P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
PI Wood WI, Wu TD;  
XX  
XX WPI: 2004-376182/35.  
DR N-PSDB; ADP54071.  
XX  
XX New PRO polynucleotides and polypeptides, useful in diagnosing  
PT and treating an immune related disease, e.g. systemic lupus  
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
PT stimulating an immune response.  
XX  
PS Claim 1; SEQ ID NO 48; 3009pp; English.  
XX  
XX The present invention describes an isolated PRO nucleic acid (I). Also  
CC described: (1) a vector comprising (1); (2) a host cell comprising the  
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
CC antibody which specifically binds to a polypeptide of (4); (7) a  
CC composition of matter comprising a polypeptide of (4), an agonist or  
CC antagonist of the polypeptide or an antibody that binds to the  
CC polypeptide in combination with a carrier; (8) an article of manufacture  
CC comprising a container, a label on the container and a composition of  
CC matter of (7); (9) a method of treating an immune related disease in a  
CC mammal; (10) a method for determining the presence of a PRO polypeptide  
CC in a sample suspected of having the polypeptide; (11) a method of  
CC diagnosing an immune related disease or an inflammatory immune response  
CC in mammal; (12) a method of identifying a compound that inhibits or  
CC mimics the activity of or expression of a gene encoding a PRO polypeptide  
CC ; and (13) a method of stimulating the immune response in a mammal. The  
CC PRO sequences have anti-allergic, antianemic, antiarthritic,  
CC antidiabetic, antidiabetic, anti-inflammatory, antipsoriatic,  
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,

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DE Mature Interleukin-1.  
 XX IL-1; cytokine; arthritis; wound healing.  
 KW Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Protein 143..295.  
 FT /label= mature IL-1  
 XX  
 PN EP456332-A.  
 XX  
 XX 13-NOV-1991.  
 XX  
 XX 13-MAR-1985; 91EP-00201769.  
 XX  
 XX 19-JUN-1984; 84US-00622201.  
 PR 27-JUL-1984; 84US-00635006.  
 XX 26-NOV-1984; 84US-00674555.  
 PR 30-NOV-1984; 84US-00676533.  
 PR 31-DEC-1984; 84US-00687646.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 XX  
 XX Cerretti DP, Conlon PJ, Cosman DJ, Grabstein KH, Hopp TP;  
 PI Kronheim SR, Larsen AD, March CJ, Price VL;  
 XX  
 DR WPI; 1991-334306/46.  
 DR N-PSDB; AAQ14647.  
 XX  
 XX DNA encoding IL-1 - used to transform hosts which express sufficient  
 PT quantities of homogeneous IL-1 or for investigations of auto-immune  
 PT diseases etc.  
 XX  
 XX Disclosure; Fig 4; 29pp; English.  
 XX  
 XX This IL-1 has biological activity in a thymocyte proliferation assay. The  
 CC sequence encoding it was derived from a cDNA clone capable of hybridising  
 CC to a specific oligonucleotide probe (see AAQ14647) after overnight  
 CC hybridisation at about 50 deg.C in 6 x saline sodium citrate. (Updated on  
 CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA  
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 295 AA;  
 SQ  
 Query Match 100.0%; Score 40; DB 2; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 DB 139 YVHDAPV 145  
 RESULT 86  
 AAY33271  
 ID AAY33271 standard; protein; 538 AA.  
 XX  
 AC AAY33271;  
 XX  
 XX 26-NOV-1999 (first entry)  
 DT  
 XX  
 XX Interleukin-1b conserved peptide fragment.  
 DE  
 XX  
 XX Interleukin-1; IL-1; cytokine; inhibitor; antagonist; receptor; trauma;  
 KW anti-inflammatory; anti-infectious; apoptotic; inflammatory; infection;  
 KW catabolic; degeneration; chronic inflammation; autoimmune disease; IL-1b;  
 KW nervous system; motor system; inhibitor; erythropoiesis; chondrocyte;  
 KW rheumatic patient; collagen synthesis; hepatocyte; cell-cell adhesion;  
 KW cartilage degradation; nerve regeneration; necrosis induction; apoptosis.  
 XX  
 OS Unidentified.  
 XX

PN DE19753753-A1.  
 XX  
 PD 26-AUG-1999.  
 XX  
 PF 04-DEC-1997; 97DE-01053753.  
 XX  
 PR 04-DEC-1997; 97DE-01053753.  
 XX  
 XX (ORTH-) ORTHOGEN GENTECHNOLOGIE GMBH.  
 XX  
 XX Meijer H, Wehling P, Reinecke J;  
 PI WPI; 1999-479917/41.  
 XX  
 DR  
 XX  
 XX New recombinant nucleic acid encoding proteins for modifying effects of  
 PT cytokine systems, e.g. for treating infection or trauma.  
 FT  
 XX  
 XX Disclosure; Fig 1; 8pp; German.  
 XX  
 XX This invention describes novel recombinant nucleic acids (I) that encode  
 CC proteins (II) which modify the effects of cytokines or their  
 CC inhibitors/antagonists or their receptors. The products of the invention  
 CC have anti-inflammatory, anti-infectious and apoptotic activity. (I) and  
 CC (II) are particularly used to modulate activities of the human  
 CC interleukin-1 (IL-1) system which is involved in many inflammatory and  
 CC catabolic processes, e.g. in infection, trauma, degeneration and chronic  
 CC inflammation (autoimmune diseases) of the nervous and motor systems and  
 CC internal organs. In particular, (II) are used in cases where IL-1  
 CC inhibits erythropoiesis in rheumatic patients, inhibits collagen  
 CC synthesis by chondrocytes, inhibits growth of hepatocytes, promotes cell-  
 CC cell adhesion, immune reactions, degradation of cartilage, nerve  
 CC regeneration, and induction of necrosis or apoptosis in the central  
 CC nervous system. This sequence represents a fragment of interleukin-1b (IL  
 CC -1b) which is used to describe the method of the invention  
 XX  
 XX Sequence 538 AA;  
 SQ  
 Query Match 100.0%; Score 40; DB 2; Length 538;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 DB 222 YVHDAPV 228  
 RESULT 87  
 AAR34852  
 ID AAR34852 standard; protein; 10 AA.  
 XX  
 AC AAR34852;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 14-JUL-1993 (first entry)  
 DT  
 XX  
 XX IL-beta protease cleavage site peptide substrate.  
 DE  
 XX  
 XX Interleukin; therapeutic; wound healing; treatment; arthritis;  
 KW autoimmune disease; radiation; side effects.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Cleavage-site 4..7  
 FT /note= "IL-beta protease cleavage site, Ala -> Gly"  
 XX  
 XX WO9305071-A1.  
 PN  
 XX 18-MAR-1993.  
 PD  
 XX 12-SEP-1991; 91WO-US006595.  
 PF  
 XX 30-AUG-1991; 91US-00750644.  
 PR

XX PA (IMMV ) IMMUNEX CORP.  
 XX PI Black RA, Sleath PR, Kronheim SR;  
 XX DR WPI; 1993-100924/12.  
 XX PT New polypeptide having protease biological activity for interleukin 1-  
 FT beta - can form inhibitor compsn. and cpds. for treatment of arthritis,  
 PT auto-immune diseases, inflammation and radiation damage; also for wound  
 PT healing.  
 XX PS Example; Page 37; 69pp; English.  
 XX CC The sequence is that of a peptide corresponding to Ala112 to Ser121 of  
 CC human precursor interleukin (IL)-1beta sequence. It contains a modified  
 CC (Ala117 -> Gly) IL-1beta protease cleavage site (His115-Pro118) for IL-  
 CC 1beta protease. It shows a reactivity of 3.40 relative to the original  
 CC sequence. (Updated on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 10 AA;  
 Query Match 90.0%; Score 36; DB 2; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 1.2;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 Db 2 YVHDGPV 8  
 |||||  
 |||||  
 RESULT 88  
 AAG73329  
 ID AAG73329 standard; peptide; 14 AA.  
 XX AC AAG73329;  
 XX DT 14-AUG-2001 (first entry)  
 XX DE Protease indicator compound peptide #58.  
 XX KW Protease detection; peptide cleavage; enzyme activity; fluorogenic;  
 KW viral infection; cancer metastasis; emphysema; arthritis; thrombosis;  
 KW haemophilia.  
 XX OS Synthetic.  
 XX PH Key Location/Qualifiers  
 FT Modified-site 4  
 FT /label= OTHER  
 FT /note= "designated J in the specification"  
 XX WO200118238-A1.  
 XX PD 15-MAR-2001.  
 XX PF 11-SEP-2000; 2000WO-US024882.  
 XX PR 10-SEP-1999; 99US-00394019.  
 XX PA (ONCO-) ONCOIMMUNIN INC.  
 XX PI Komoriya A, Packard BS;  
 XX DR WPI; 2001-389573/41.  
 XX CC New fluorogenic compositions whose fluorescence level increases in the  
 FT presence of active proteases, useful for detecting and localizing  
 PT protease activity in biological samples, particularly in frozen tissue  
 PT samples.  
 XX PS Claim 4; Page 71; 86pp; English.  
 XX

CC The present invention describes fluorogenic compositions which can be  
 CC used for the detection of protease activity. This can be useful as an  
 CC indicator of viral infection, cancer metastasis, haemophilia, emphysema,  
 CC thrombosis and arthritis. The fluorogenic compositions comprise a  
 CC peptide, a peptide spacer and a donor and an acceptor fluorophore. The  
 CC peptide is cleaved by a protease and the fluorophores can then be  
 CC detected. The present sequence is one of the peptides described in the  
 CC exemplification of the invention  
 XX SQ Sequence 14 AA;  
 Query Match 90.0%; Score 36; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAP 6  
 Db 6 YVHDAP 11  
 |||||  
 |||||  
 RESULT 89  
 AAU10757  
 ID AAU10757 standard; peptide; 14 AA.  
 XX AC AAU10757;  
 XX DT 12-MAR-2002 (first entry)  
 XX DE Target peptide sequence used in Far Western blot protocol.  
 XX KW Peptide-peptide interaction; library encoded peptide; LEP; EBM;  
 KW DNA binding domain; prokaryotic operator region; chip-based technology;  
 KW epitope binding molecule; substrate-directed inhibition;  
 KW lambda repressor reconstitution system; Far Western blot protocol.  
 XX OS Synthetic.  
 XX PN US2001029024-A1.  
 XX PD 11-OCT-2001.  
 XX PF 09-FEB-2001; 2001US-00780575.  
 XX PR 11-FEB-2000; 2000US-0182060P.  
 XX PA (KODA/) KODADEK T J.  
 XX PI Kodadek TJ;  
 XX DR WPI; 2001-647984/74.  
 XX PT Identifying peptide-peptide interaction comprises identifying library  
 FT encoded peptide as partner to target peptide if complex having first and  
 FT second DNA binding domains fused to the peptides, binds to prokaryotic  
 FT operator.  
 XX PS Disclosure; Fig 5; 33pp; English.  
 XX CC The present invention relates to a method of identifying peptide-peptide  
 CC interactions. The method comprises contacting first, second fusion  
 CC constructs containing target peptide or library encoded peptide (LSP)  
 CC fused to first, second DNA binding domains respectively, in a prokaryotic  
 CC host cell containing a prokaryotic operator region, and determining  
 CC binding of the complex. The method is useful for screening a peptide  
 CC library for peptide-peptide interactions. The LSP selected by the method  
 CC is useful as capture probes for a specific target protein to which it  
 CC binds, and for controlling the post translational modification of the  
 CC proteins in a novel fashion. The LSPs identified by the method can be  
 CC employed as epitope binding molecules (EBM). The high affinity epitope  
 CC binding molecules can be used as capture agents in chip-based  
 CC technologies. The identified LSPs are also useful in a novel application  
 CC termed substrate-directed inhibition by which substrate-targeted  
 CC inhibitors are identified by the present method. The LSPs may serve as

CC lead compounds for the development of non-peptidic small molecule  
 CC analogues, or may be used directly as drugs. The method provides a highly  
 CC sensitive screening assay for the identification of peptide binding  
 CC partners to virtually any peptide or polypeptide ligand. The lambda  
 CC repressor reconstitution system described is sensitive to even low  
 CC affinity interactions. The present sequence for a target peptide sequence  
 CC is used in a Far Western blot protocol in the methods of the present  
 CC invention

XX Sequence 14 AA;  
 SQ Query Match 90.0%; Score 36; DB 4; Length 14;  
 Best Local Similarity 85.7%; Pred. No. 1.7;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 4 YVHDGFPV 10  
 |||||

RESULT 90  
 AAU10760  
 ID AAU10760 standard; peptide; 14 AA.

XX AC AAU10760;

XX DT 12-MAR-2002 (first entry)

XX DE LEPB substrate, peptide GG.

XX KW Peptide-peptide interaction; library encoded peptide; LEP; EBM;  
 KW DNA binding domain; prokaryotic operator region; chip-based technology;  
 KW epitope binding molecule; substrate-directed inhibition; GST; GFP;  
 KW lambda repressor reconstitution system; glutathione S-transferase;  
 KW green fluorescent protein.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Attached to glutathione S-transferase (GST)"

FT Modified-site 14

FT /note= "Attached to green fluorescent protein (GFP)"

XX US2001029024-A1.

XX 11-OCT-2001.

XX 09-FEB-2001; 2001US-00780575.

XX 11-FEB-2000; 2000US-0182060P.

XX (KODAK/) KODADEK T J.

XX Kodadek TJ;

XX WPI; 2001-647984/74.

XX Identifying peptide-peptide interaction comprises identifying library  
 PT encoded peptide as partner to target peptide if complex having first and  
 PT second DNA binding domains fused to the peptides, binds to prokaryotic  
 PT operator.

XX Example; Fig 8; 33pp; English.

XX The present invention relates to a method of identifying peptide-peptide  
 CC interactions. The method comprises contacting first, second fusion  
 CC constructs containing target peptide or library encoded peptide (LEP)  
 CC fused to first, second DNA binding domains respectively, in a prokaryotic  
 CC host cell containing a prokaryotic operator region, and determining  
 CC binding of the complex. The method is useful for screening a peptide  
 CC library for peptide-peptide interactions. The LEP selected by the method  
 CC is useful as capture probes for a specific target protein to which it

CC binds, and for controlling the post translational modification of the  
 CC proteins in a novel fashion. The LEPs identified by the method can be  
 CC employed as epitope binding molecules (EBM). The high affinity epitope  
 CC binding molecules can be used as capture agents in chip-based  
 CC technologies. The identified LEPs are also useful in a novel application  
 CC termed substrate-directed inhibition by which substrate-targeted  
 CC inhibitors are identified by the present method. The LEPs may serve as  
 CC lead compounds for the development of non-peptidic small molecule  
 CC analogues, or may be used directly as drugs. The method provides a highly  
 CC sensitive screening assay for the identification of peptide binding  
 CC partners to virtually any peptide or polypeptide ligand. The lambda  
 CC repressor reconstitution system described is sensitive to even low  
 CC affinity interactions. The present sequence represents peptide GG which  
 CC acts as a LEPB substrate in the methods of the present invention

XX SQ Sequence 14 AA;

Query Match 90.0%; Score 36; DB 4; Length 14;  
 Best Local Similarity 85.7%; Pred. No. 1.7;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 4 YVHDGFPV 10  
 |||||

RESULT 91  
 AAR06358  
 ID AAR06358 standard; protein; 268 AA.

XX AC AAR06358;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 13-DEC-1990 (first entry)

XX DE Monkey IL-2 beta deduced from cDNA.

XX KW Interleukin.

XX OS Cebus apella.

XX PN JP02177885-A.

XX PD 10-JUL-1990.

XX PF 28-DEC-1988; 88JP-00332467.

XX PR 28-DEC-1988; 88JP-00332467.

XX (SAKA ) OTSUKA PHARM CO LTD.

XX WPI; 1990-252053/33.

DR N-PSDB; AAQ05593.

XX PT Monkey IL-beta gene - obtd. by introducing recombinant plasmid into host  
 PT cells which are incubated.

XX Disclosure; Page 3; 13pp; Japanese.

XX The gene encoding the protein can be used to produce recombinant monkey  
 CC IL-2 beta. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-  
 CC AUG-2003 to correct OS field.)

XX SQ Sequence 268 AA;

Query Match 90.0%; Score 36; DB 2; Length 268;  
 Best Local Similarity 85.7%; Pred. No. 38;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 113 FVHDAPV 119  
 :|||||

## RESULT 92

ADN88476  
ID ADN88476 standard; peptide; 16 AA.

AC ADN88476;

DT 12-AUG-2004 (first entry)

DE Fluorogenic protease indicator peptide #172.

KW fluorogenic; protease detection; protease inhibitor.

XX Synthetic.

OS US2004096926-A1.

PN 20-MAY-2004.

XX 04-JUN-2001; 2001US-00874350.

XX 20-FEB-1997; 97US-00802981.

PR 20-FEB-1998; 98WO-US003000.

PR 10-SEP-1999; 99US-00394019.

PR 11-SEP-2000; 2000WO-US024882.

XX (ONCO-) ONCOIMMUNIN INC.

XX Packard BS, Komoriya A;

XX WPI; 2004-399235/37.

XX Fluorogenic composition useful for detecting protease activity and test

PS Disclosure; SEQ ID NO 172; 114pp; English.

CC The invention relates to a fluorogenic composition (I) for detecting the  
CC activity of a protease. (I) is useful for detecting the activity of a  
CC protease, which involves contacting the protease with (I), where the  
CC activity of protease is detected in a histological section, cell culture  
CC or tissue section. The cell suspension is derived from the biological  
CC sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The  
CC protease activity is detected by fluorescence microscopy, fluorescence  
CC microplate reader, absorption microplate reader, flow cytometry,  
CC fluorometry, absorption spectroscopy or confocal fluorescent microplate  
CC reader. (I) is useful for delivering a molecule into a cell, and for  
CC screening a test agent for the ability to modulate the activity of the  
CC protease. (I) is useful for detection and localisation of protease  
CC activity in biological samples. (I) also acts as a protease inhibitor,  
CC thus useful as protease inhibitors. (I) enables detection of the protease  
CC activity, and provides a high intensity fluorescent signal at a visible  
CC wavelength when they are digested by a protease. The present sequence  
CC represents a fluorogenic protease indicator peptide of the invention.

XX Sequence 16 AA;

SQ Query Match

82.5%; Score 33; DB 8; Length 16;

Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7

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5 VHDAPV 10

## RESULT 93

AAH88306

ID AAH88306 standard; protein; 83 AA.

XX

AC AAH88306;

XX

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen SEQ ID NO:15899.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytostatic; gene therapy; vaccine; metastasis.

OS Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 14-AUG-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225277P.

PR 14-AUG-2000; 2000US-0225758P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 06-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.





DR WPI; 2003-533017/50.  
 DR N-PSDB; ADB68947.  
 XX  
 PT New nucleic acid, useful for preparing a composition for treating an  
 PT infection caused by *Cryptococcus neoformans*.  
 XX  
 PS Claim 9; SEQ ID NO 3074; 136pp; English.  
 XX  
 XX The invention relates to a novel purified or isolated *Cryptococcus*  
 CC *neoformans* nucleic acid molecule comprising a sequence encoding a  
 CC polypeptide comprising a sequence not given in the specification. A  
 CC polynucleotide of the invention has fungicide activity, and may have a  
 CC use in gene therapy. The nucleic acid is useful for preparing a  
 CC composition for treating an infection caused by *Cryptococcus neoformans*.  
 CC The present sequence represents a *C. neoformans* sequence of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published\\_pat\\_sequences](http://ftp.wipo.int/pub/published_pat_sequences).  
 XX  
 SQ Sequence 272 AA;

Query Match 82.5%; Score 33; DB 7; Length 272;  
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 DB 77 YLHDCPV 83  
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RESULT 95  
 AAU72965  
 ID AAU72965 standard; protein; 419 AA.  
 XX  
 AC AAU72965;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE *Neisseria meningitidis* virulence protein #55.  
 XX  
 KW Meningitis; virulence; gene; antibacterial; vaccine; veterinary;  
 KW infection; Gram-negative bacteria; antimicrobial.  
 OS *Neisseria meningitidis*.  
 XX  
 PN WO200185772-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 08-MAY-2001; 2001WO-GB002003.  
 XX  
 PR 08-MAY-2000; 2000GB-00011108.  
 XX  
 PA (MICR-) MICROSCIENCE LTD.  
 XX  
 PI Tang C;  
 XX  
 DR WPI; 2002-066593/09.  
 DR N-PSDB; AAS97250.  
 XX  
 PT New peptide encoded by operon including virulence genes of *Neisseria*  
 PT meningitidis, useful as vaccine component for treating or preventing  
 PT meningitis and for identifying antimicrobial drug.  
 XX  
 PS Claim 4; Page 235-236; 423pp; English.  
 XX  
 XX The invention relates to a peptide (I) encoded by an operon (II) of  
 CC *Neisseria meningitidis* including virulence genes, or a related molecule  
 CC having a 40% sequence similarity at the peptide or nucleotide level in a  
 CC Gram-negative bacterium, or its functional fragment, for therapeutic or  
 CC diagnostic use. (I) and (II) are useful in the manufacture of a  
 CC medicament for treating or preventing a condition (e.g., meningitis)  
 CC associated with infection by *Neisseria* or Gram-negative bacteria. The  
 XX product is useful for veterinary treatment and in a screening assay for  
 PT meningitis, useful as vaccine component for treating or preventing  
 PT meningitis and for identifying antimicrobial drug.  
 XX  
 PS Claim 4; Page 235-236; 423pp; English.

CC product is useful for veterinary treatment and in a screening assay for  
 CC the identification of an antimicrobial drug. The vaccines have  
 CC prophylactic applications. AAU72911-AAU73014 represent *N. meningitidis*  
 CC virulence proteins of the invention  
 XX  
 SQ Sequence 419 AA;

Query Match 82.5%; Score 33; DB 5; Length 419;  
 Best Local Similarity 71.4%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 DB 315 YVHDVPL 321  
 |||||

RESULT 96  
 AAU72938  
 ID AAU72938 standard; protein; 419 AA.  
 XX  
 AC AAU72938;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE *Neisseria meningitidis* virulence protein #28.  
 XX  
 KW Meningitis; virulence; gene; antibacterial; vaccine; veterinary;  
 KW infection; Gram-negative bacteria; antimicrobial.  
 OS *Neisseria meningitidis*.  
 XX  
 PN WO200185772-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 08-MAY-2001; 2001WO-GB002003.  
 XX  
 PR 08-MAY-2000; 2000GB-00011108.  
 XX  
 PA (MICR-) MICROSCIENCE LTD.  
 XX  
 PI Tang C;  
 XX  
 DR WPI; 2002-066593/09.  
 DR N-PSDB; AAS97223.  
 XX  
 PT New peptide encoded by operon including virulence genes of *Neisseria*  
 PT meningitidis, useful as vaccine component for treating or preventing  
 PT meningitis and for identifying antimicrobial drug.  
 XX  
 PS Claim 4; Page 119-120; 423pp; English.  
 XX  
 XX The invention relates to a peptide (I) encoded by an operon (II) of  
 CC *Neisseria meningitidis* including virulence genes, or a related molecule  
 CC having a 40% sequence similarity at the peptide or nucleotide level in a  
 CC Gram-negative bacterium, or its functional fragment, for therapeutic or  
 CC diagnostic use. (I) and (II) are useful in the manufacture of a  
 CC medicament for treating or preventing a condition (e.g., meningitis)  
 CC associated with infection by *Neisseria* or Gram-negative bacteria. The  
 CC product is useful for veterinary treatment and in a screening assay for  
 CC the identification of an antimicrobial drug. The vaccines have  
 CC prophylactic applications. AAU72911-AAU73014 represent *N. meningitidis*  
 CC virulence proteins of the invention  
 XX  
 SQ Sequence 419 AA;

Query Match 82.5%; Score 33; DB 5; Length 419;  
 Best Local Similarity 71.4%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 DB 315 YVHDVPL 321  
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RESULT 97
ABG24306
ID ABG24306 standard; protein; 451 AA.
XX
XX
AC ABG24306;
XX
XX
DT 18-FEB-2002 (first entry)
XX
XX
DE Novel human diagnostic protein #24297.
XX
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200175067-A2.
XX
XX
PD 11-OCT-2001.
XX
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
XX
PR 31-MAR-2000; 2000US-00540217.
XX
XX
PR 23-AUG-2000; 2000US-00649167.
XX
XX
PA (HYSE-) HYSEQ INC.
XX
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX
DR WPI; 2001-639362/73.
XX
XX
DR N-PSDB; AAS88493.
XX
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX
PS Claim 20; SEQ ID NO 54665; 103pp; English.
XX
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 451 AA;
XX
XX
Query Match 82.5%; Score 33; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 2 VHDAPV 7
DB 441 VHDAPV 446
|||||
KW Interleukin; therapeutic; wound healing; treatment; arthritis;
KW autoimmune disease; radiation; side effects.
XX
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RESULT 98
ABB72034
ID ABB72034 standard; protein; 1172 AA.
XX
XX
AC ABB72034;
XX
XX
DT 26-MAR-2002 (first entry)
XX
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 42894.
XX
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX
OS Drosophila melanogaster.
XX
XX
PN WO200171042-A2.
XX
XX
PD 27-SEP-2001.
XX
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
XX
PR 11-JUL-2000; 2000US-00614150.
XX
XX
PA (PEKE ) PE CORP NY.
XX
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX
DR WPI; 2001-656860/75.
XX
XX
DR N-PSDB; ABL16137.
XX
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
XX
PS Disclosure; SEQ ID NO 42894; 21pp + Sequence Listing; English.
XX
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABLO1840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 1172 AA;
XX
XX
Query Match 82.5%; Score 33; DB 4; Length 1172;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX
QY 1 YVHDAPV 7
DB 672 YLHDSPI 678
|||||
XX
XX
RESULT 99
AAR34854
ID AAR34854 standard; protein; 10 AA.
XX
XX
AC AAR34854;
XX
XX
DT 25-MAR-2003 (revised)
DT 14-JUL-1993 (first entry)
XX
XX
DE IL-beta protease cleavage site peptide substrate.
XX
XX
KW Interleukin; therapeutic; wound healing; treatment; arthritis;
KW autoimmune disease; radiation; side effects.
XX
```

OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Cleavage-site 4..7  
 FT /note= "IL-beta protease cleavage site, Pro -> Ala"  
 FT  
 PN WC9305071-A1.  
 XX 18-MAR-1993.  
 PD  
 XX  
 XX 12-SEP-1991; 91WO-US006595.  
 XX  
 XX 30-AUG-1991; 91US-00750644.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 XX  
 XX Black RA, Sleath PR, Kronheim SR;  
 XX  
 XX WPI; 1993-100924/12.  
 XX  
 XX New polypeptide having protease biological activity for interleukin 1-  
 PT beta - can form inhibitor compsn. and cpds. for treatment of arthritis,  
 PT auto:immune diseases, inflammation and radiation damage; also for wound  
 PT healing.  
 XX  
 XX Example; Page 37; 69pp; English.  
 PS  
 XX The sequence is that of a peptide corresponding to Ala112 to Ser121 of  
 CC human precursor interleukin (IL)-beta sequence. It contains a modified  
 CC (Pro118 -> Ala) IL-beta protease cleavage site (His115-Pro118) for IL-  
 CC beta protease. It shows a reactivity of 0.47 relative to the original  
 CC sequence. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 80.0%; Score 32; DB 2; Length 10;  
 Best Local Similarity 85.7%; Pred. No. 7.9;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 |||||  
 Db 2 YVHDAV 8  
 RESULT 100  
 AAB43346  
 ID AAB43346 standard; protein; 179 AA.  
 XX  
 AC AAB43346;  
 XX  
 XX 08-FEB-2001 (first entry)  
 XX  
 XX Human ORFX ORF3110 polypeptide sequence SEQ ID NO:6220.  
 XX  
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
 KW vulnery; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200058473-A2.  
 XX

PD 05-OCT-2000.  
 XX 31-MAR-2000; 2000WO-US008621.  
 XX  
 PR 31-MAR-1999; 99US-0127607P.  
 PR 02-APR-1999; 99US-0127636P.  
 PR 05-APR-1999; 99US-0127728P.  
 PR 30-MAR-2000; 2000US-00540763.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX  
 XX Shimkets RA, Leach M;  
 XX  
 XX WPI; 2000-602362/57.  
 DR N-PSDB; AAC7555.  
 DR  
 XX  
 XX Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease.  
 XX  
 XX Claim 11; Page 5405; 5507pp; English.  
 XX  
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
 CC antipsoriatic; antiparkinsonian; neurotropic; neuroprotective; osteopathic;  
 CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;  
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;  
 CC dermatological; immunosuppressive; antiinflammatory; antibacterial;  
 CC antiviral; antifungal; antirheumatic; antithyroid; and antianemic. The  
 CC sequences can be used for determining the presence of or predisposition  
 CC to, or preventing or treating pathological conditions associated with an  
 CC ORFX-associated disorder. The nucleic acids can be used to express ORFX  
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be  
 CC used to treat cancers, proliferative disorders, neurodegenerative  
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,  
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester  
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency  
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune  
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and  
 CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to  
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive  
 XX  
 XX Sequence 179 AA;  
 Query Match 80.0%; Score 32; DB 3; Length 179;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAP 6  
 |||||  
 Db 58 YIHDS 63

Search completed: June 30, 2005, 22:19:47  
 Job time : 172 secs

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OM protein - protein search, using sw model

Run on: June 30, 2005, 22:19:55 ; Search time 42 Seconds  
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Title: US-09-874-350C-210

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Sequence: 1 YVHDAPV 7

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

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6: /cgn2\_6/prodata/1/iaa/backfiles1 pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	40	100.0	8	1	US-08-440-179-22
3	40	100.0	8	3	US-09-039-657-22
4	40	100.0	10	1	US-08-203-716-13
5	40	100.0	10	1	US-08-385-434-7
6	40	100.0	10	1	US-08-649-197-7
7	40	100.0	10	1	US-08-440-179-13
8	40	100.0	10	2	US-08-748-117A-1
9	40	100.0	10	2	US-08-597-346-1
10	40	100.0	10	2	US-08-679-350-1
11	40	100.0	10	3	US-09-039-657-13
12	40	100.0	10	4	US-09-421-954-1
13	40	100.0	10	6	5422425-8
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15	40	100.0	12	1	US-06-203-716-21
16	40	100.0	12	1	US-08-440-179-21
17	40	100.0	12	3	US-09-039-657-21
18	40	100.0	13	3	US-09-117-608-2
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20	40	100.0	14	3	US-08-665-643A-2
21	40	100.0	17	1	US-08-385-434-11
22	40	100.0	17	1	US-08-649-197-11
23	40	100.0	17	6	5422425-12
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25	40	100.0	269	1	US-08-203-716-3
26	40	100.0	269	1	US-08-440-179-3
27	40	100.0	269	2	US-08-432-693-11

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30	40	100.0	269	3	US-09-211-290-11	Sequence 11, Appl
31	40	100.0	269	3	US-09-030-613-11	Sequence 11, Appl
32	40	100.0	269	3	US-09-322-676-11	Sequence 11, Appl
33	40	100.0	269	3	US-09-039-657-3	Sequence 3, Appl
34	40	100.0	269	3	US-08-748-547-4	Sequence 4, Appl
35	40	100.0	269	3	US-09-466-036A-11	Sequence 11, Appl
36	40	100.0	269	3	US-09-451-905-11	Sequence 11, Appl
37	40	100.0	269	4	US-09-949-016-5960	Sequence 5960, Ap
38	40	100.0	269	5	PCT-US91-02339-1	Sequence 1, Appl
39	40	100.0	298	4	US-09-949-016-11362	Sequence 11362, A
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42	36	90.0	10	1	US-08-203-716-18	Sequence 18, Appl
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45	36	90.0	10	1	US-08-440-179-18	Sequence 18, Appl
46	36	90.0	10	3	US-09-039-657-15	Sequence 15, Appl
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51	35	87.5	10	3	US-09-039-657-14	Sequence 14, Appl
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57	33	82.5	10	3	US-09-039-657-16	Sequence 16, Appl
58	32	80.0	10	1	US-08-203-716-20	Sequence 20, Appl
59	32	80.0	10	1	US-08-440-179-20	Sequence 20, Appl
60	32	80.0	10	3	US-09-039-657-20	Sequence 20, Appl
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62	32	80.0	422	4	US-09-134-000C-5643	Sequence 5643, Ap
63	32	80.0	914	3	US-09-437-054A-8	Sequence 8, Appl
64	31	77.5	10	1	US-08-203-716-19	Sequence 19, Appl
65	31	77.5	10	1	US-08-440-179-19	Sequence 19, Appl
66	31	77.5	10	3	US-09-039-657-19	Sequence 19, Appl
67	31	77.5	60	4	US-10-179-784-20	Sequence 20, Appl
68	31	77.5	60	4	US-10-179-784-22	Sequence 22, Appl
69	31	77.5	481	4	US-09-543-681A-8321	Sequence 8321, Ap
70	31	77.5	1090	4	US-09-252-991A-23149	Sequence 23149, A
71	30	75.0	60	4	US-10-179-784-9	Sequence 9, Appl
72	30	75.0	221	4	US-09-270-767-57481	Sequence 57481, A
73	30	75.0	338	4	US-09-270-767-42208	Sequence 42208, A
74	30	75.0	548	4	US-09-252-991A-21629	Sequence 21629, A
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77	30	75.0	816	4	US-09-540-236-3443	Sequence 3443, Ap
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80	29	72.5	107	4	US-09-281-760E-36	Sequence 36, Appl
81	29	72.5	121	4	US-09-252-991A-23454	Sequence 23454, A
82	29	72.5	145	4	US-09-543-681A-5202	Sequence 5202, Ap
83	29	72.5	178	4	US-09-252-991A-20957	Sequence 20957, A
84	29	72.5	179	4	US-09-107-532A-7290	Sequence 7290, Ap
85	29	72.5	183	4	US-09-252-991A-19320	Sequence 19320, A
86	29	72.5	205	4	US-09-949-016-7376	Sequence 7376, Ap
87	29	72.5	218	1	US-08-417-822A-2	Sequence 2, Appl
88	29	72.5	242	4	US-09-252-991A-28448	Sequence 28448, A
89	29	72.5	245	4	US-09-489-039A-9197	Sequence 9197, Ap
90	29	72.5	254	4	US-09-489-039A-7881	Sequence 7881, Ap
91	29	72.5	263	4	US-09-724-797-12	Sequence 12, Appl
92	29	72.5	274	4	US-09-489-039A-13000	Sequence 13000, A
93	29	72.5	289	4	US-09-248-796A-17294	Sequence 17294, A
94	29	72.5	296	4	US-09-270-767-33591	Sequence 33591, A
95	29	72.5	312	4	US-09-701-623C-2	Sequence 2, Appl
96	29	72.5	340	4	US-09-270-767-58348	Sequence 58348, A
97	29	72.5	345	4	US-09-252-991A-33007	Sequence 33007, A
98	29	72.5	349	4	US-09-328-352-7606	Sequence 7606, Ap
99	29	72.5	354	4	US-09-543-681A-6524	Sequence 6524, Ap
100	29	72.5	368	4	US-09-538-092-1226	Sequence 1226, Ap

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101 29 72.5 376 4 US-09-107-532A-6913 Sequence 6913, Ap
102 29 72.5 386 4 US-09-270-767-41410 Sequence 4140, A
103 29 72.5 386 4 US-09-270-767-56626 Sequence 56626, A
104 29 72.5 390 4 US-09-902-540-12046 Sequence 12046, A
105 29 72.5 418 4 US-09-949-016-10645 Sequence 10645, A
106 29 72.5 413 4 US-09-252-991A-32677 Sequence 32677, A
107 29 72.5 426 5 PCT-US95-13795-2 Sequence 2, Appli
108 29 72.5 426 4 US-09-595-857B-28 Sequence 28, Appl
109 29 72.5 439 4 US-09-328-352-4576 Sequence 4576, Ap
110 29 72.5 477 4 US-09-270-767-43020 Sequence 43020, A
111 29 72.5 495 4 US-09-902-540-11210 Sequence 11210, A
112 29 72.5 497 3 US-08-869-696-9 Sequence 9, Appli
113 29 72.5 556 3 US-08-869-696-2 Sequence 2, Appli
114 29 72.5 582 3 US-09-091-725-17 Sequence 17, Appl
115 29 72.5 607 4 US-09-489-039A-12140 Sequence 12140, A
116 29 72.5 613 1 US-08-272-875-3 Sequence 3, Appli
117 29 72.5 613 4 US-09-543-681A-5298 Sequence 5298, Ap
118 29 72.5 806 1 US-08-270-076A-11 Sequence 11, Appl
119 29 72.5 907 4 US-09-252-991A-24114 Sequence 24114, A
120 29 72.5 998 2 US-08-415-788-7 Sequence 7, Appli
121 29 72.5 1029 2 US-08-415-788-3 Sequence 3, Appli
122 29 72.5 1131 4 US-09-248-796A-19110 Sequence 19110, A
123 29 72.5 1233 3 US-09-194-613-5 Sequence 5, Appli
124 29 72.5 1343 4 US-09-270-767-31792 Sequence 31792, A
125 29 72.5 1343 4 US-09-270-767-47009 Sequence 47009, A
126 29 72.5 1501 4 US-09-252-991A-20266 Sequence 20266, A
127 29 71.2 295 4 US-09-543-681A-5406 Sequence 5406, Ap
128 28.5 70.0 6 3 US-08-953-033-8 Sequence 8, Appli
129 28 70.0 6 4 US-08-877-605-145 Sequence 145, App
130 28 70.0 8 3 US-08-953-033-6 Sequence 6, Appli
131 28 70.0 8 3 US-08-953-033-7 Sequence 7, Appli
132 28 70.0 8 3 US-08-953-033-10 Sequence 10, Appl
133 28 70.0 8 3 US-08-953-033-15 Sequence 15, Appl
134 28 70.0 8 3 US-08-953-033-16 Sequence 16, Appl
135 28 70.0 8 3 US-08-953-033-17 Sequence 17, Appl
136 28 70.0 11 1 US-08-594-447-19 Sequence 19, Appl
137 28 70.0 11 1 US-08-541-964-18 Sequence 18, Appl
138 28 70.0 11 2 US-08-665-647-33 Sequence 33, Appl
139 28 70.0 14 3 US-08-953-033-23 Sequence 23, Appl
140 28 70.0 77 4 US-09-389-956-20 Sequence 20, Appl
141 28 70.0 110 4 US-09-389-956-8 Sequence 8, Appli
142 28 70.0 118 4 US-09-302-540-11433 Sequence 11433, A
143 28 70.0 137 4 US-09-389-956-22 Sequence 22, Appl
144 28 70.0 177 4 US-09-325-932A-170 Sequence 170, App
145 28 70.0 205 3 US-09-248-796A-27103 Sequence 27103, A
146 28 70.0 211 4 US-08-857-076-113 Sequence 113, App
147 28 70.0 211 4 US-09-328-352-5475 Sequence 5475, Ap
148 28 70.0 212 4 US-09-270-767-32555 Sequence 32555, A
149 28 70.0 212 4 US-09-270-767-47772 Sequence 47772, A
150 28 70.0 212 4
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## ALIGNMENTS

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RESULT 1
US-08-203-716-22
; Sequence 22, Application US/08203716
; Patent No. 5416013
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
; STREET: 180 N. STETSON
; CITY: CHICAGO
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/203,716
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/750,644
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KATZ, MARTIN L.
; REGISTRATION NUMBER: 25011
; REFERENCE/DOCKET NUMBER: IMMUNEX2108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165400
; TELEFAX: 3126165400
; TELEX: 9102211206
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-203-716-22

Query Match 100.0%; Score 40; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 1 YVHDAPV 7

RESULT 2
US-08-440-179-22
; Sequence 22, Application US/08440179
; Patent No. 5756465
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
; STREET: 180 N. STETSON
; CITY: CHICAGO
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,179
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,644
; FILING DATE: 30-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: KATZ, MARTIN L.
; REGISTRATION NUMBER: 25011
; REFERENCE/DOCKET NUMBER: IMMUNEX2108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165400
; TELEFAX: 3126165400
```

; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-440-179-22

Query Match 100.0%; Score 40; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 1 YVHDAPV 7

RESULT 3  
US-09-039-657-22  
; Sequence 22, Application US/09039657  
; Patent No. 6136787  
; GENERAL INFORMATION:  
; APPLICANT: Black, Roy A.  
; APPLICANT: Sleath, Paul R.  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
; TITLE OF INVENTION: 1B PROTEASE INHIBITORS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,657  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-657-22

Query Match 100.0%; Score 40; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 1 YVHDAPV 7

RESULT 4  
US-08-203-716-13  
; Sequence 13, Application US/08203716

; Patent No. 5416013  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/203,716  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/750,644  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25011  
REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-203-716-13

Query Match 100.0%; Score 40; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 2 YVHDAPV 8

RESULT 5  
US-08-385-434-7  
; Sequence 7, Application US/08385434  
; Patent No. 5545518  
; GENERAL INFORMATION:  
; APPLICANT: Krieglner, Michael  
; APPLICANT: Nitecki, Danute, E.  
; TITLE OF INVENTION: Assay For Determining TNF or IL-1 Convertase  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation, Intellectual Property R440  
; STREET: P.O. Box 8097  
; CITY: Emeryville  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/385,434
/ FILING DATE: 08-FEB-95
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/562,720
/ FILING DATE: 06-AUG-1990
/ APPLICATION DATA: 08/053,558
/ FILING DATE: 26-APR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pochopien, Donald J.
/ REGISTRATION NUMBER: 32,167
/ REFERENCE/DOCKET NUMBER: 32386/871.003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/474-6300
/ TELEFAX: 312/474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-385-434-7

Query Match 100.0%; Score 40; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 2 YVHDAPV 8

RESULT 6
US-08-649-197-7
/ Sequence 7, Application US/08649197
/ Patent No. 563593
/ GENERAL INFORMATION:
/ APPLICANT: Kriegler, Michael
/ APPLICANT: Nitecki, Danute, E.
/ TITLE OF INVENTION: Methods For The Identification Of Cytokine
/ TITLE OF INVENTION: Convertase Inhibitors
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Chiron Corporation, Intellectual Property R440
/ STREET: P.O. Box 8097
/ CITY: Emeryville
/ STATE: California
/ COUNTRY: United States of America
/ ZIP: 94662-8097
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/649,197
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/385,434
/ FILING DATE: 08-FEB-95
/ APPLICATION DATA:
/ APPLICATION NUMBER: 07/562,720
/ FILING DATE: 06-AUG-1990
/ APPLICATION DATA: 08/053,558
/ FILING DATE: 26-APR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Savereide, Paul B.
/ REGISTRATION NUMBER: 36,914

/ REFERENCE/DOCKET NUMBER: 33296/0871.004
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (510) 601-2585
/ TELEFAX: (510) 655-3542
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-649-197-7

Query Match 100.0%; Score 40; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 2 YVHDAPV 8

RESULT 7
US-08-440-179-13
/ Sequence 13, Application US/08440179
/ Patent No. 5756465
/ GENERAL INFORMATION:
/ APPLICANT: BLACK, ROY A
/ APPLICANT: SLEATH, PAUL R
/ APPLICANT: KRONHEIM, SHIRLEY R
/ TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
/ ADDRESSEE: MILNAMOW
/ STREET: 180 N. STETSON
/ CITY: CHICAGO
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/440,179
/ FILING DATE: 12-MAY-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/750,644
/ FILING DATE: 30-AUG-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KATZ, MARTIN L.
/ REGISTRATION NUMBER: 25011
/ REFERENCE/DOCKET NUMBER: IMMUNEX2108
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 3126165400
/ TELEFAX: 3126165460
/ TELEX: 9102211206
/ INFORMATION FOR SEQ ID NO: 13:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-440-179-13

Query Match 100.0%; Score 40; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 2 YVHDAPV 8
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Db 2 YVHDAPV 8

RESULT 8  
US-08-748-117A-1  
; Sequence 1, Application US/08748117A  
; Patent No. 5834514  
; GENERAL INFORMATION:  
; APPLICANT: Dolle, Roland E.  
; APPLICANT: Rinker, James M.  
; TITLE OF INVENTION: HALOMETHYL AMIDES AS IL-1 BETA PROTEASE  
; TITLE OF INVENTION: INHIBITORS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr.  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/748,117A  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 564  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/453,122  
; FILING DATE: 30-MAY-1995  
; PRIOR APPLICATION DATA: US 08/236,425  
; FILING DATE: 29-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: VPI/SW/010 DIV CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /note= "alanine is derivatized with TRITC - tetramethylrhodamine isothiocyanate"  
; OTHER INFORMATION: isothiocyanate"  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 10  
; OTHER INFORMATION: /product= "OTHER"  
; OTHER INFORMATION: /note= "serine carboxylic acid is derivatized as an amide"  
US-08-748-117A-1

Query Match 100.0%; Score 40; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHDAPV 8

RESULT 9

US-08-597-346-1  
; Sequence 1, Application US/08597346  
; Patent No. 5843905  
; GENERAL INFORMATION:  
; APPLICANT: Dolle, Roland E.  
; APPLICANT: Singh, Jasbir  
; APPLICANT: Speier, Gary  
; TITLE OF INVENTION: Peptidic Phosphorylketones as Interleukin  
; TITLE OF INVENTION: 1a-Converting Enzyme  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterling Winthrop Inc.  
; STREET: 9 Great Valley Parkway  
; STREET: P.O. Box 3026  
; CITY: Malvern  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19355  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Macintosh 7.1  
; SOFTWARE: Microsoft Word 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/597,346  
; FILING DATE: 06-FEB-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/248,791  
; FILING DATE: May 25, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doreen M. Wells  
; REGISTRATION NUMBER: 34,278  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 889-8684  
; TELEFAX: (610) 889-6364  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: -1  
; OTHER INFORMATION: /label= TRITC  
; OTHER INFORMATION: /note= "TRITC is tetramethylrhodamine isothiocyanate".  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 11  
; OTHER INFORMATION: /label= Xaa  
; OTHER INFORMATION: /note= "Xaa is NH2".  
US-08-597-346-1

Query Match 100.0%; Score 40; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHDAPV 8

RESULT 10  
US-08-679-350-1  
; Sequence 1, Application US/08679350  
; Patent No. 5985838  
; GENERAL INFORMATION:  
; APPLICANT: Ator, Mark A.  
; APPLICANT: Awad, Mohamed M.A.  
; APPLICANT: Chaturvedula, Prasad V.  
; APPLICANT: Dolle, Roland E.

APPLICANT: Hoyer, Denton W.  
APPLICANT: Lodge, Eric P.  
APPLICANT: Osifo, Irennegbe K.  
APPLICANT: Prouty, Catherine, P.  
APPLICANT: Rinker, James M.  
APPLICANT: Ross, Tina Morgan  
APPLICANT: Salvino, Joseph M.  
APPLICANT: Schmidt, Stanley J.  
APPLICANT: Singh, Jasbir  
TITLE OF INVENTION: PEPTIDE ANALOGS AS IRREVERSIBLE  
TITLE OF INVENTION: INTERLEUKIN-1 (PROTEASE INHIBITORS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sanofi Winthrop, Inc.  
STREET: 9 Great Valley Parkway  
CITY: Malvern  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19355  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage  
COMPUTER: Compaq Deskpro XL466  
OPERATING SYSTEM: Windows For Workgroups 3.11  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/679,350  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/371,723  
FILING DATE: 12 January 1995  
APPLICATION NUMBER: 08/055,051  
FILING DATE: 29 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: William J. Davis  
REGISTRATION NUMBER: 30,744  
REFERENCE/DOCKET NUMBER: 62040-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 889-8802  
TELEFAX: (610) 889-8799  
TELEX: No. 59858386  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 Amino Acids  
TYPE: Amino Acid  
STRANDEDNESS:  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: -1  
OTHER INFORMATION: /label=TRITC  
OTHER INFORMATION: /note="TRITC is tetramethylrhodamine isothiocyanate".  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION:  
US-08-679-350-1  
Query Match 100.0%; Score 40; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
Db 2 YVHDAPV 8  
RESULT 11  
US-09-039-657-13  
Sequence 13, Application US/09039657  
Patent No. 6136787  
GENERAL INFORMATION:  
APPLICANT: Black, Roy A.

APPLICANT: Sleath, Paul R.  
APPLICANT: Kronheim, Shirley R.  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
TITLE OF INVENTION: 1B PROTEASE INHIBITORS  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,657  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-657-13  
Query Match 100.0%; Score 40; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
Db 2 YVHDAPV 8  
RESULT 12  
US-09-421-954-1  
Sequence 1, Application US/09421954  
Patent No. 6576614  
GENERAL INFORMATION:  
APPLICANT: Ator, Mark A.  
APPLICANT: Awad, Mohamed M.A.  
APPLICANT: Chaturvedula, Prasad V.  
APPLICANT: Dolle, Roland E.  
APPLICANT: Hoyer, Denton W.  
APPLICANT: Lodge, Eric P.  
APPLICANT: Osifo, Irennegbe K.  
APPLICANT: Prouty, Catherine, P.  
APPLICANT: Rinker, James M.  
APPLICANT: Ross, Tina Morgan  
APPLICANT: Salvino, Joseph M.  
APPLICANT: Schmidt, Stanley J.  
APPLICANT: Singh, Jasbir  
TITLE OF INVENTION: PEPTIDE ANALOGS AS IRREVERSIBLE  
TITLE OF INVENTION: INTERLEUKIN-1 (PROTEASE INHIBITORS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sanofi Winthrop, Inc.  
STREET: 9 Great Valley Parkway  
CITY: Malvern  
STATE: Pennsylvania  
COUNTRY: USA

ZIP: 19355  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage  
COMPUTER: Compaq Deskpro XL466  
OPERATING SYSTEM: Windows For Workgroups 3.11  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/421,954  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/679,350  
FILING DATE:  
APPLICATION NUMBER: 08/055,051  
FILING DATE: 29 April 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: William J. Davis  
REGISTRATION NUMBER: 30,744  
REFERENCE/DOCKET NUMBER: 62040-2  
TELEPHONE: (610) 889-8802  
TELEFAX: (610) 889-8799  
TELEX: NO. 6576614e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 Amino Acids  
TYPE: Amino Acid  
STRANDEDNESS:  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: -1  
OTHER INFORMATION: /label=TRITC  
OTHER INFORMATION: /note="TRITC is tetramethylrhodamine isothiocyanate".  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11  
OTHER INFORMATION:  
US-09-421-954-1

Query Match 100.0%; Score 40; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
Db 2 YVHDAVP 8

RESULT 13  
5422425-8  
; Patent No. 5422425  
; APPLICANT: KRIEGLER, MICHAEL; NITECKI, DANUTE E.  
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF CYTOKINE  
; CONVERTASE INHIBITORS  
; NUMBER OF SEQUENCES: 12  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/53,558  
; FILING DATE: 26-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 562,720  
; FILING DATE: 06-AUG-1990  
; SEQ ID NO: 8:  
; LENGTH: 10  
5422425-8

Query Match 100.0%; Score 40; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
Db 2 YVHDAVP 8

RESULT 14  
5422425-8  
; Patent No. 5422425  
; APPLICANT: KRIEGLER, MICHAEL; NITECKI, DANUTE E.  
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF CYTOKINE  
; CONVERTASE INHIBITORS  
; NUMBER OF SEQUENCES: 12  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/53,558  
; FILING DATE: 26-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 562,720  
; FILING DATE: 06-AUG-1990  
; SEQ ID NO: 8:  
; LENGTH: 10  
5422425-8

Query Match 100.0%; Score 40; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
Db 2 YVHDAVP 8

RESULT 15  
US-08-203-716-21  
; Sequence 21, Application US/08203716  
; Patent No. 5416013  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/203,716  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/750,644  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011  
; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3126165400  
; TELEFAX: 3126165460  
; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-203-716-21

Query Match 100.0%; Score 40; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.062; 0; Indels 0;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 3 YVHDAPV 9

RESULT 16  
US-08-440-179-21  
; Sequence 21, Application US/08440179  
; Patent No. 5756465  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; ADDRESSEE: MILNAMOW  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,179  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/750,644  
; FILING DATE: 30-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011  
; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3126165400  
; TELEFAX: 3126165460  
; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-440-179-21

Query Match 100.0%; Score 40; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.062; 0; Indels 0;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 3 YVHDAPV 9

RESULT 17  
US-09-039-657-21  
; Sequence 21, Application US/09039657  
; Patent No. 6136787  
; GENERAL INFORMATION:  
; APPLICANT: Black, Roy A.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Kronheim, Shirley R.  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN

; TITLE OF INVENTION: 1B PROTEASE INHIBITORS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,657  
; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: VPI/SW002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-039-657-21

Query Match 100.0%; Score 40; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.062;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 3 YVHDAPV 9

RESULT 18  
US-09-117-608-2  
; Sequence 2, Application US/09117608  
; Patent No. 6166202  
; GENERAL INFORMATION:  
; APPLICANT: Simmonds, Adrian  
; APPLICANT: Miller, James N.  
; APPLICANT: Moody, Christopher J.  
; APPLICANT: Swann, Elizabeth  
; APPLICANT: Briggs, Mark S.J.  
; APPLICANT: Bruce, Ian E.  
; TITLE OF INVENTION: BENZOPHENOXAZINE DYES  
; FILE REFERENCE: 28911/34892  
; CURRENT APPLICATION NUMBER: US/09/117,608  
; CURRENT FILING DATE: 1999-01-15  
; PRIOR APPLICATION NUMBER: 9602265.2 GB  
; PRIOR FILING DATE: 1996-02-05  
; PRIOR APPLICATION NUMBER: PCT/GB97/00324  
; PRIOR FILING DATE: 1997-02-05  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-117-608-2

Query Match 100.0%; Score 40; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.067; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 2 YVHDAPV 8

## RESULT 19

US-08-354-685-3  
; Sequence 3, Application US/08354685  
; Patent No. 5498695  
; GENERAL INFORMATION:  
; APPLICANT: Daumy, Gaston O.  
; TITLE OF INVENTION: PARA-NITROANILIDE PEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Peter C. Richardson  
; STREET: 235 East 42nd Street, 20th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10017-5755  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/354,685  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 981,153  
; FILING DATE: 24-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Strassburger, Philip C.  
; REGISTRATION NUMBER: 34,258  
; REFERENCE/DOCKET NUMBER: PC8352  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)573-5731  
; TELEFAX: (212)573-1939  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

## US-08-354-685-3

Query Match 100.0%; Score 40; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.072; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 4 YVHDAPV 10

## RESULT 20

US-08-665-643A-2  
; Sequence 2, Application US/08665643A  
; Patent No. 6288037  
; GENERAL INFORMATION:  
; APPLICANT: Talanian, Robert V.  
; APPLICANT: Ghayur, Tariq  
; APPLICANT: Hodges, John C.  
; TITLE OF INVENTION: SUBSTRATES AND INHIBITORS FOR CYSTEINE PROTEASE ICH-1  
; FILE REFERENCE: BBI-049CPCPA  
; CURRENT APPLICATION NUMBER: US/08/665,643A

; CURRENT FILING DATE: 1996-06-18  
; PRIOR APPLICATION NUMBER: 08/592,943  
; PRIOR FILING DATE: 1996-01-29  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; OTHER INFORMATION: amino-terminal acetyl modification;  
; OTHER INFORMATION: carboxy-terminal amide modification  
; US-08-665-643A-2

Query Match 100.0%; Score 40; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.072; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 4 YVHDAPV 10

## RESULT 21

US-08-385-434-11  
; Sequence 11, Application US/08385434  
; Patent No. 5545518  
; GENERAL INFORMATION:  
; APPLICANT: Kriegler, Michael  
; APPLICANT: Nitecki, Danute, E.  
; TITLE OF INVENTION: Assay For Determining TNP or IL-1 Convertase  
; TITLE OF INVENTION: Activity  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation, Intellectual Property R440  
; STREET: P.O. Box 8097  
; CITY: Emeryville  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94662-8097  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/385,434  
; FILING DATE: 08-FEB-95  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/562,720  
; FILING DATE: 06-AUG-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/053,558  
; FILING DATE: 26-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pochopien, Donald J.  
; REGISTRATION NUMBER: 32,167  
; REFERENCE/DOCKET NUMBER: 32386/871.003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site

LOCATION: 11.15  
OTHER INFORMATION: /note= "The residue at this  
OTHER INFORMATION: location is beta-alanine"  
US-08-385-434-11

Query Match 100.0%; Score 40; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAV 7  
Db 2 YVHDAV 8

RESULT 23  
US-08-649-197-11  
Patent No. 5639593  
GENERAL INFORMATION:  
APPLICANT: Kriegluer, Michael, E.  
APPLICANT: Nitecki, Danute, E.  
TITLE OF INVENTION: Methods For The Identification Of Cytokine  
TITLE OF INVENTION: Convertase Inhibitors  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation, Intellectual Property R440  
STREET: P.O. Box 8097  
CITY: Emeryville  
STATE: California  
COUNTRY: United States of America  
ZIP: 94662-8097  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/649,197  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/385,434  
FILING DATE: 08-FEB-95  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/582,720  
FILING DATE: 06-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/053,558  
FILING DATE: 26-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Savereide, Paul B.  
REGISTRATION NUMBER: 36,914  
REFERENCE/DOCKET NUMBER: 33296/0871.004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2585  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 11.15  
OTHER INFORMATION: /note= "The residue at this  
OTHER INFORMATION: location is beta-alanine"  
US-08-649-197-11

Query Match 100.0%; Score 40; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.089; 0; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAV 7  
Db 2 YVHDAV 8

RESULT 23  
5422425-12  
Patent No. 5422425  
APPLICANT: KRIEGLER, MICHAEL; NITECKI, DANUTE E.  
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF CYTOKINE  
CONVERTASE INHIBITORS  
NUMBER OF SEQUENCES: 12  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/53,558  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 562,720  
FILING DATE: 06-AUG-1990  
SEQ ID NO:12:  
LENGTH: 17  
5422425-12

Query Match 100.0%; Score 40; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAV 7  
Db 2 YVHDAV 8

RESULT 24  
5422425-12  
Patent No. 5422425  
APPLICANT: KRIEGLER, MICHAEL; NITECKI, DANUTE E.  
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF CYTOKINE  
CONVERTASE INHIBITORS  
NUMBER OF SEQUENCES: 12  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/53,558  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 562,720  
FILING DATE: 06-AUG-1990  
SEQ ID NO:12:  
LENGTH: 17  
5422425-12

Query Match 100.0%; Score 40; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.089;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAV 7  
Db 2 YVHDAV 8

RESULT 25  
US-08-203-716-3  
Sequence 3, Application US/08203716  
Patent No. 5416013  
GENERAL INFORMATION:  
APPLICANT: BLACK, ROY A  
APPLICANT: SLEATH, PAUL R  
APPLICANT: KRONHEIM, SHIRLEY R  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
STREET: 180 N. STETSON  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA

ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/203,716  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/750,644  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25011  
REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-203-716-3

Query Match 100.0%; Score 40; DB 1; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAV 7  
Db 113 YVHDAV 119

RESULT 26  
US-08-440-179-3  
Sequence 3, Application US/08440179  
Patent No. 5756465  
GENERAL INFORMATION:  
APPLICANT: BLACK, ROY A  
APPLICANT: SLEATH, PAUL R  
APPLICANT: KRONHEIM, SHIRLEY R  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
ADDRESS: MILANOW  
STREET: 180 N. STETSON  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,179  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,644  
FILING DATE: 30-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25011  
REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-440-179-3

Query Match 100.0%; Score 40; DB 1; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAV 7  
Db 113 YVHDAV 119

RESULT 27  
US-08-432-693-11  
Sequence 11, Application US/08432693  
Patent No. 5861267  
GENERAL INFORMATION:  
APPLICANT: Su, Michael  
TITLE OF INVENTION: METHODS AND HOST CELLS FOR ASSAYING  
EXOGENOUS AND ENDOGENOUS PROTEASE ACTIVITY  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432,693  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr, James F  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/95-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-432-693-11

Query Match 100.0%; Score 40; DB 2; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAV 7  
Db 113 YVHDAV 119

RESULT 28  
US-08-599-895-11  
Sequence 11, Application US/08599895  
Patent No. 5891855

;; GENERAL INFORMATION:  
;; APPLICANT: Florikiewicz, Robert Z.  
;; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
;; NUMBER OF SEQUENCES: 13  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SEED and BERRY LLP  
;; STREET: 6300 Columbia Center, 701 Fifth Avenue  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: USA  
;; ZIP: 98104-7092  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/599,895  
;; FILING DATE: 31-JAN-1996  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: No. 5891855tenburg Ph.D., Carol  
;; REGISTRATION NUMBER: 39,317  
;; REFERENCE/DOCKET NUMBER: 760100.416  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206) 622-4900  
;; TELEFAX: (206) 682-6031  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 269 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-599-895-11

Query Match 100.0%; Score 40; DB 2; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 113 YVHDAPV 119

RESULT 29  
US-08-483-806-2  
; Sequence 2, Application US/08483806  
; Patent No. 5985657  
; GENERAL INFORMATION:  
; APPLICANT: Auron, Philip E.  
; APPLICANT: Dinarello, Charles A.  
; APPLICANT: Webb, Andrew C.  
; APPLICANT: Rich, Alexander  
; APPLICANT: Wolff, Sheldon M.  
; TITLE OF INVENTION: Recombinant DNA Which Codes for  
; INTERLEUKIN-1  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Saliwanchik & Saliwanchik  
; STREET: 2421 N.W. 41st Street  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 32606-6669  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/483,806  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/071,031  
;; FILING DATE: 01-JUN-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/880,476  
;; FILING DATE: 06-MAY-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/557,279  
;; FILING DATE: 24-JUL-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/185,731  
;; FILING DATE: 25-APR-1988  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/004,319  
;; FILING DATE: 18-JAN-1987  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 06/611,669  
;; FILING DATE: 18-MAY-1984  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lloyd, Jeff  
;; REGISTRATION NUMBER: 35,589  
;; REFERENCE/DOCKET NUMBER: N100FDDFD1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (352) 375-8100  
;; TELEFAX: (352) 372-5800  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 269 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-483-806-2

Query Match 100.0%; Score 40; DB 2; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 113 YVHDAPV 119

RESULT 30  
US-09-211-290-11  
; Sequence 11, Application US/09211290  
; Patent No. 6071885  
; GENERAL INFORMATION:  
; APPLICANT: Florikiewicz, Robert Z.  
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/211,290  
; FILING DATE: 12-DEC-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 200124.401D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900



```

; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-211-290-11

Query Match 100.0%; Score 40; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 113 YVHDAPV 119

RESULT 31
US-09-030-613-11
; Sequence 11, Application US/09030613
; Patent No. 6083706
; GENERAL INFORMATION:
; APPLICANT: Florkiewicz, Robert Z.
; APPLICANT: Baird, J. Andrew
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,613
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6083706tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-030-613-11

Query Match 100.0%; Score 40; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 113 YVHDAPV 119

RESULT 32
US-09-322-676-11
; Sequence 11, Application US/09322676
; Patent No. 6107283
; GENERAL INFORMATION:
; APPLICANT: Florkiewicz, Robert Z.
; APPLICANT: Florkiewicz, Robert Z.
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/322,676
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/211,290
; FILING DATE: 12-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 200124.401D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-322-676-11

Query Match 100.0%; Score 40; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 113 YVHDAPV 119

RESULT 33
US-09-039-657-3
; Sequence 3, Application US/09039657
; Patent No. 6136787
; GENERAL INFORMATION:
; APPLICANT: Black, Roy A.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Kronheim, Shirley R.
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN
; TITLE OF INVENTION: 1B PROTEASE INHIBITORS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,657
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
```

NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-039-657-3

Query Match 100.0%; Score 40; DB 3; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 113 YVHDAPV 119

RESULT 34  
US-08-748-547-4  
Sequence 4, Application US/08748547  
Patent No. 6187550  
GENERAL INFORMATION:  
APPLICANT: GHAYUR, TARIO  
APPLICANT: MCGUINNESS, LORRAINE M.  
TITLE OF INVENTION: METHODS AND CELL LINES FOR SCREENING  
TITLE OF INVENTION: COMPOSITIONS AND GENES FOR ABILITY TO INTERACT WITH IL-1B  
TITLE OF INVENTION: AND ICE PROCESSING  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
STREET: 600 ATLANTIC AVENUE  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/748,547  
FILING DATE: 13-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/280,889  
FILING DATE: 27-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: JANIUK, ANTHONY J.  
REGISTRATION NUMBER: 29,809  
REFERENCE/DOCKET NUMBER: B0870/7000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-720-3500  
TELEFAX: 617-720-2441  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-748-547-4

Query Match 100.0%; Score 40; DB 3; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 113 YVHDAPV 119

RESULT 35  
US-09-466-036A-11  
Sequence 11, Application US/09466036A  
Patent No. 6281197  
GENERAL INFORMATION:  
APPLICANT: Florikiewicz, Robert Z.  
TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/466,036A  
FILING DATE: 17-Dec-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/211,290  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 200124.401D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-466-036A-11

Query Match 100.0%; Score 40; DB 3; Length 269;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 113 YVHDAPV 119

RESULT 36  
US-09-451-905-11  
Sequence 11, Application US/09451905  
Patent No. 6306613  
GENERAL INFORMATION:  
APPLICANT: Robert Z. Florikiewicz  
APPLICANT: Andrew Baird  
APPLICANT: Dale E. Warnock  
TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME  
FILE REFERENCE: 200124.402C4  
CURRENT APPLICATION NUMBER: US/09/451,905  
CURRENT FILING DATE: 1999-12-01  
NUMBER OF SEQ ID NOS: 48  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11

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; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-451-905-11

Query Match 100.0%; Score 40; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 113 YVHDAPV 119

RESULT 37
US-09-949-016-5960
; Sequence 5960, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5960
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5960

Query Match 100.0%; Score 40; DB 4; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 113 YVHDAPV 119

RESULT 38
PCT-US91-02339-1
; Sequence 1, Application PC/TUS9102339
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY
; APPLICANT: SLEATH, PAUL
; APPLICANT: KRONHEIM, SHIRLEY
; TITLE OF INVENTION: INTERLEUKIN 1 B PROTEASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02339
; FILING DATE: 19910404
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: OSTER, JEFFREY B.
; REGISTRATION NUMBER: 32,585
; REFERENCE/DOCKET NUMBER: 0401WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2065870430
; TELEFAX: 2065870606
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: INTERLEUKIN-1B
PCT-US91-02339-1

Query Match 100.0%; Score 40; DB 5; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 113 YVHDAPV 119

RESULT 39
US-09-949-016-11362
; Sequence 11362, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11362
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11362

Query Match 100.0%; Score 40; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 142 YVHDAPV 148

RESULT 40
US-08-203-716-15
; Sequence 15, Application US/08203716
; Patent No. 5416013
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
; STREET: 180 N. STETSON
```

;; CITY: CHICAGO  
;; STATE: IL  
;; COUNTRY: USA  
;; ZIP: 60601  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.24  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/203,716  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/750,644  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: KATZ, MARTIN L.  
;; REGISTRATION NUMBER: 25011  
;; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 3126165400  
;; TELEFAX: 3126165460  
;; TELEX: 9102211206  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-203-716-15

Query Match 90.0%; Score 36; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
Db 2 YVHEAPV 8

RESULT 41  
US-08-203-716-17  
; Sequence 17, Application US/08203716  
; Patent No. 5416013  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/203,716  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/750,644  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011

;; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 3126165400  
;; TELEFAX: 3126165460  
;; TELEX: 9102211206  
;; INFORMATION FOR SEQ ID NO: 17:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-203-716-17

Query Match 90.0%; Score 36; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
Db 2 YVHDGPV 8

RESULT 42  
US-08-203-716-18  
; Sequence 18, Application US/08203716  
; Patent No. 5416013  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/203,716  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/750,644  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011  
; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3126165400  
; TELEFAX: 3126165460  
; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-203-716-18

Query Match 90.0%; Score 36; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||

Db 2 YVHDPV 8

## RESULT 43

US-08-440-179-15  
; Sequence 15, Application US/08440179  
; Patent No. 5756465  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; ADDRESSEE: MILNAMOW  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,179  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/750,644  
; FILING DATE: 30-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011  
; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3126165400  
; TELEFAX: 3126165460  
; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-440-179-15

Query Match 90.0%; Score 36; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDPV 7  
Db 2 YVHEAPV 8

## RESULT 44

US-08-440-179-17  
; Sequence 17, Application US/08440179  
; Patent No. 5756465  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; ADDRESSEE: MILNAMOW  
; STREET: 180 N. STETSON  
; CITY: CHICAGO

STATE: IL  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,179  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,644  
FILING DATE: 30-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25011  
REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-440-179-17

Query Match 90.0%; Score 36; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDPV 7  
Db 2 YVHDPV 8

## RESULT 45

US-08-440-179-18  
; Sequence 18, Application US/08440179  
; Patent No. 5756465  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; ADDRESSEE: MILNAMOW  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,179  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/750,644  
; FILING DATE: 30-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011

REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-440-179-18

Query Match 90.0%; Score 36; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
||| |||  
Db 2 YVHDAVP 8

## RESULT 46

US-09-039-657-15  
Sequence 15, Application US/09039657  
Patent No. 6136787  
GENERAL INFORMATION:  
APPLICANT: Black, Roy A.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Kronheim, Shirley R.  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,657  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELEPHONE: 212-596-9090  
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-657-15

Query Match 90.0%; Score 36; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
||| |||  
Db 2 YVHDAVP 8

## RESULT 47

US-09-039-657-17  
Sequence 17, Application US/09039657  
Patent No. 6136787  
GENERAL INFORMATION:  
APPLICANT: Black, Roy A.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Kronheim, Shirley R.  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,657  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELEPHONE: 212-596-9090  
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-657-17

Query Match 90.0%; Score 36; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
||| |||  
Db 2 YVHDAVP 8

## RESULT 48

US-09-039-657-18  
Sequence 18, Application US/09039657  
Patent No. 6136787  
GENERAL INFORMATION:  
APPLICANT: Black, Roy A.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Kronheim, Shirley R.  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,657  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELEPHONE: 212-596-9090  
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-657-15

Query Match 90.0%; Score 36; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.33;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
||| |||  
Db 2 YVHDAVP 8

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,657
; FILING DATE: 16-MAR-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: VPI/SW002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-039-657-18

Query Match          90.0%; Score 36; DB 3; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.33;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDPV 7
        |||||
Db      2 YVHDPV 8

RESULT 49
US-08-203-716-14
; Sequence 14, Application US/08203716
; Patent No. 5416013
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
; STREET: 180 N. STETSON
; CITY: CHICAGO
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/07/750,644
; FILING DATE:
; APPLICATION NUMBER: US/07/750,644
; ATTORNEY/AGENT INFORMATION:
; NAME: KATZ, MARTIN L.
; REGISTRATION NUMBER: 25011
; REFERENCE/DOCKET NUMBER: IMMUNEX2108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165400
; TELEFAX: 3126165460
; TELEX: 9102211206
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-203-716-14

Query Match          87.5%; Score 35; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDPV 7
        |||||
Db      2 YVHDPV 8

RESULT 51
US-09-039-657-14
; Sequence 14, Application US/09039657
; Patent No. 6136787
; GENERAL INFORMATION:
```

```
;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-020-716-14

Query Match          87.5%; Score 35; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDPV 7
        |||||
Db      2 YVHDPV 8

RESULT 50
US-08-440-179-14
; Sequence 14, Application US/08440179
; Patent No. 5756465
; GENERAL INFORMATION:
; APPLICANT: BLACK, ROY A
; APPLICANT: SLEATH, PAUL R
; APPLICANT: KRONHEIM, SHIRLEY R
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &
; STREET: 180 N. STETSON
; CITY: CHICAGO
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 07/750,644
; FILING DATE: 30-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: KATZ, MARTIN L.
; REGISTRATION NUMBER: 25011
; REFERENCE/DOCKET NUMBER: IMMUNEX2108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3126165400
; TELEFAX: 3126165460
; TELEX: 9102211206
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-440-179-14

Query Match          87.5%; Score 35; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.53;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDPV 7
        |||||
Db      2 YVHDPV 8

RESULT 51
US-09-039-657-14
; Sequence 14, Application US/09039657
; Patent No. 6136787
; GENERAL INFORMATION:
```

APPLICANT: Black, Roy A.  
APPLICANT: Sleath, Paul R.  
APPLICANT: Kronheim, Shirley R.  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,657  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-657-14

Query Match 87.5%; Score 35; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 0.53;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHNPV 8

RESULT 52  
US-08-203-716-23  
Sequence 23, Application US/08203716  
Patent No. 5416013  
GENERAL INFORMATION:  
APPLICANT: BLACK, ROY A  
APPLICANT: SLEATH, PAUL R  
APPLICANT: KRONHEIM, SHIRLEY R  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
STREET: 180 N. STETSON  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/203,716  
FILING DATE:  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/750,644  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25011  
REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-203-716-23

Query Match 82.5%; Score 33; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
Db 1 VHDAPV 6

RESULT 53  
US-08-440-179-23  
Sequence 23, Application US/08440179  
Patent No. 5756465  
GENERAL INFORMATION:  
APPLICANT: BLACK, ROY A  
APPLICANT: SLEATH, PAUL R  
APPLICANT: KRONHEIM, SHIRLEY R  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
ADDRESSEE: MILNAMOW  
STREET: 180 N. STETSON  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA  
ZIP: 60601

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,179  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,644  
FILING DATE: 30-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25011  
REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-440-179-23



Query Match 82.5%; Score 33; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
Db 1 VHDAPV 6

RESULT 54  
US-09-039-657-23  
; Sequence 23, Application US/09039657  
; Patent No. 6136787  
; GENERAL INFORMATION:  
; APPLICANT: Black, Roy A.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Kronheim, Shirley R.  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
; TITLE OF INVENTION: 1B PROTEASE INHIBITORS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,657  
; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: VPI/SW002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-039-657-23

Query Match 82.5%; Score 33; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
Db 1 VHDAPV 6

RESULT 55  
US-08-203-716-16  
; Sequence 16, Application US/08203716  
; Patent No. 5416013  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/203,716  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/750,644  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011  
; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3126165400  
; TELEFAX: 3126165460  
; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; LOCATION: 4  
; IDENTIFICATION METHOD: Xaa = D-Asp  
US-08-203-716-16

Query Match 82.5%; Score 33; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHXAPV 8

RESULT 56  
US-08-440-179-16  
; Sequence 16, Application US/08440179  
; Patent No. 5756465  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; ADDRESS: MILANOW  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,179  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/750,644  
;; FILING DATE: 30-AUG-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: KATZ, MARTIN L.  
;; REGISTRATION NUMBER: 25011  
;; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 3126165400  
;; TELEFAX: 3126165460  
;; TELEX: 9102211206  
;; INFORMATION FOR SEQ ID NO: 16:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; LOCATION: 4  
;; IDENTIFICATION METHOD: Xaa = D-Asp  
US-08-440-179-16

Query Match 82.5%; Score 33; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHXAPV 8

RESULT 57  
US-09-039-657-16  
; Sequence 16, Application US/09039657  
; Patent No. 6136787  
; GENERAL INFORMATION:  
; APPLICANT: Black, Roy A.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Kronheim, Shirley R.  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
; TITLE OF INVENTION: 1B PROTEASE INHIBITORS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,657  
; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: VPI/SW002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:

;; NAME/KEY: Modified-site  
;; LOCATION: 5  
;; OTHER INFORMATION: /product= "D-Asp"  
US-09-039-657-16

Query Match 82.5%; Score 33; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHXAPV 8

RESULT 58  
US-08-203-716-20  
; Sequence 20, Application US/08203716  
; Patent No. 5416013  
; GENERAL INFORMATION:  
; APPLICANT: Black, Roy A.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Kronheim, Shirley R.  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER GOLDSMITH, SHORE, SUTKER &  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/203,716  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/750,644  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011  
; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3126165400  
; TELEFAX: 3126165460  
; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-203-716-20

Query Match 80.0%; Score 32; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 2.2;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHDAV 8

RESULT 59  
US-08-440-179-20  
; Sequence 20, Application US/08440179  
; Patent No. 5756465  
; GENERAL INFORMATION:

APPLICANT: BLACK, ROY A  
APPLICANT: SLEATH, PAUL R  
APPLICANT: KRONHEIM, SHIRLEY R  
TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
ADDRESSEE: MILINAWOW  
STREET: 180 N. STETSON  
CITY: CHICAGO  
STATE: IL  
COUNTRY: USA  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,179  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,644  
FILING DATE: 30-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: KATZ, MARTIN L.  
REGISTRATION NUMBER: 25011  
REFERENCE/DOCKET NUMBER: IMMUNEX2108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 3126165400  
TELEFAX: 3126165460  
TELEX: 9102211206  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-440-179-20

Query Match 80.0%; Score 32; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 2.2;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHDAV 8  
|||||

RESULT 60  
US-09-039-657-20  
; Sequence 20, Application US/09039657  
; Patent No. 6136787  
; GENERAL INFORMATION:  
; APPLICANT: Black, Roy A.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Kronheim, Shirley R.  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,657  
FILING DATE: 16-MAR-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: VPI/SW002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-039-657-20

Query Match 80.0%; Score 32; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 2.2;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVHDAV 8  
|||||

RESULT 61  
US-09-134-001C-4198  
; Sequence 4198, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4198  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4198

Query Match 80.0%; Score 32; DB 3; Length 223;  
Best Local Similarity 57.1%; Pred. No. 56;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 171 YVHDFPI 177  
|:|:|

RESULT 62  
US-09-134-000C-5643  
; Sequence 5643, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5643  
; LENGTH: 422  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-5643

Query Match 80.0%; Score 32; DB 4; Length 422;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
Db 295 IHDPV 300

## RESULT 63

US-09-437-054A-8  
; Sequence 8, Application US/09437054A  
; Patent No. 6316698  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Stephen M.  
; APPLICANT: Kinney, Anthony J.  
; TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs  
; FILE REFERENCE: BB1273 US NA  
; CURRENT APPLICATION NUMBER: US/09/437,054A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/107,909  
; PRIOR FILING DATE: 1998-No. 6316698member-10  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 8  
; LENGTH: 914  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-09-437-054A-8

Query Match 80.0%; Score 32; DB 3; Length 914;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
Db 257 YIHDP 262

## RESULT 64

US-08-203-716-19  
; Sequence 19, Application US/08203716  
; Patent No. 5416013  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/203,716  
; FILING DATE:  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/750,644  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011  
; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3126165400  
; TELEFAX: 3126165460  
; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-203-716-19

Query Match 77.5%; Score 31; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 3.5;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVFDAPV 8

## RESULT 65

US-08-440-179-19  
; Sequence 19, Application US/08440179  
; Patent No. 5756465  
; GENERAL INFORMATION:  
; APPLICANT: BLACK, ROY A  
; APPLICANT: SLEATH, PAUL R  
; APPLICANT: KRONHEIM, SHIRLEY R  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DRESSLER, GOLDSMITH, SHORE, SUTKER &  
; ADDRESSEE: MILNAMOW  
; STREET: 180 N. STETSON  
; CITY: CHICAGO  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,179  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/750,644  
; FILING DATE: 30-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KATZ, MARTIN L.  
; REGISTRATION NUMBER: 25011  
; REFERENCE/DOCKET NUMBER: IMMUNEX2108  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3126165400  
; TELEFAX: 3126165460  
; TELEX: 9102211206  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-440-179-19

Query Match 77.5%; Score 31; DB 1; Length 10;  
Best Local Similarity 85.7%; Pred. No. 3.5;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVFDAPV 8

## RESULT 66

US-09-039-657-19  
; Sequence 19, Application US/09039657  
; Patent No. 6136787  
; GENERAL INFORMATION:  
; APPLICANT: Black, Roy A.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Kronheim, Shirley R.  
; TITLE OF INVENTION: INTERLEUKIN 1B PROTEASE AND INTERLEUKIN  
; TITLE OF INVENTION: 1B PROTEASE INHIBITORS  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FISH & NEAVE  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,657  
; FILING DATE: 16-MAR-1998  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haley Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: VPI/SW002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-039-657-19

Query Match 77.5%; Score 31; DB 3; Length 10;  
Best Local Similarity 85.7%; Pred. No. 3.5;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 2 YVFDAPV 8

## RESULT 67

US-10-179-784-20  
; Sequence 20, Application US/10179784  
; Patent No. 6787341  
; GENERAL INFORMATION:  
; APPLICANT: Shuman, Stewart  
; APPLICANT: Striskanda, Verl  
; TITLE OF INVENTION: Pharmacological Targeting of Bacterial DNA Ligase  
; TITLE OF INVENTION: For Treatment And Prevention of Bacterial Infections  
; FILE REFERENCE: D6468  
; CURRENT APPLICATION NUMBER: US/10/179,784

; CURRENT FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: US 60/300,727  
; PRIOR FILING DATE: 2001-06-24  
; NUMBER OF SEQ ID NOS: 41  
; SEQ ID NO 20  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Mycobacterium leprae  
; FEATURE:  
; NAME/KEY: DOMAIN  
; OTHER INFORMATION: domain Ia of NAD+-dependent DNA ligase  
US-10-179-784-20

Query Match 77.5%; Score 31; DB 4; Length 60;  
Best Local Similarity 71.4%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 15 YVRDAPV 21

## RESULT 68

US-10-179-784-22  
; Sequence 22, Application US/10179784  
; Patent No. 6787341  
; GENERAL INFORMATION:  
; APPLICANT: Shuman, Stewart  
; APPLICANT: Striskanda, Verl  
; TITLE OF INVENTION: Pharmacological Targeting of Bacterial DNA Ligase  
; TITLE OF INVENTION: For Treatment And Prevention of Bacterial Infections  
; FILE REFERENCE: D6468  
; CURRENT APPLICATION NUMBER: US/10/179,784  
; CURRENT FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: US 60/300,727  
; PRIOR FILING DATE: 2001-06-24  
; NUMBER OF SEQ ID NOS: 41  
; SEQ ID NO 22  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; NAME/KEY: DOMAIN  
; OTHER INFORMATION: domain Ia of NAD+-dependent DNA ligase  
US-10-179-784-22

Query Match 77.5%; Score 31; DB 4; Length 60;  
Best Local Similarity 71.4%; Pred. No. 23;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 15 YVRDAPV 21

## RESULT 69

US-09-543-681A-8321  
; Sequence 8321, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709,1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 8321  
; LENGTH: 481  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis

US-09-543-681A-8321

Query Match 77.5%; Score 31; DB 4; Length 481;  
Best Local Similarity 71.4%; Pred. No. 26+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|.:|:|:|  
Db 5 YMHAPV 11

RESULT 70

US-09-252-991A-23149  
; Sequence 23149, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23149  
; LENGTH: 1090  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23149

Query Match 77.5%; Score 31; DB 4; Length 1090;  
Best Local Similarity 83.3%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|:|  
Db 753 YFHDAP 758

RESULT 71

US-10-179-784-9  
; Sequence 9, Application US/10179784  
; Patent No. 6787341  
; GENERAL INFORMATION:  
; APPLICANT: Shuman, Stewart  
; APPLICANT: Sriekanda, Verl  
; TITLE OF INVENTION: Pharmacological Targeting of Bacterial DNA Ligase  
; FILE REFERENCE: D6468  
; CURRENT APPLICATION NUMBER: US/10/179,784  
; CURRENT FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: US 60/300,727  
; PRIOR FILING DATE: 2001-06-24  
; NUMBER OF SEQ ID NOS: 41  
; SEQ ID NO 9  
; LENGTH: 60  
; TYPE: PRT  
; ORGANISM: Bordetella pertussis  
; FEATURE:  
; NAME/KEY: DOMAIN  
; OTHER INFORMATION: domain Ia of NAD+-dependent DNA ligase  
US-10-179-784-9

Query Match 75.0%; Score 30; DB 4; Length 60;  
Best Local Similarity 83.3%; Pred. No. 36;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|:|  
Db 15 YVHDDP 20

RESULT 72

US-09-270-767-57481  
; Sequence 57481, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57481  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-57481

Query Match 75.0%; Score 30; DB 4; Length 221;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|:|  
Db 51 YVHDAGI 57

RESULT 73

US-09-270-767-42208  
; Sequence 42208, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42208  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-42208

Query Match 75.0%; Score 30; DB 4; Length 338;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|:|  
Db 168 YVHDAGI 174

RESULT 74

US-09-252-991A-21629  
; Sequence 21629, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21629

; LENGTH: 548  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21629

Query Match 75.0%; Score 30; DB 4; Length 548;  
Best Local Similarity 66.7%; Pred. No. 3.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|  
Db 468 YLHDSF 473

## RESULT 75

US-09-543-681A-4969  
; Sequence 4969, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:

; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 4969  
; LENGTH: 700  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-4969

Query Match 75.0%; Score 30; DB 4; Length 700;  
Best Local Similarity 83.3%; Pred. No. 4.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|  
Db 471 YQHDAP 476

## RESULT 76

US-08-062-368-4  
; Sequence 4, Application US/08062368  
; Patent No. 5491086  
; GENERAL INFORMATION:

; APPLICANT: Gelfand, David H.  
; APPLICANT: Wang, Alice M.  
; TITLE OF INVENTION: Purified Thermostable Nucleic Acid  
; TITLE OF INVENTION: Polymerases Enzyme From Pyrodictum Species  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann-La Roche Inc.  
; STREET: 340 Kingsland Street  
; CITY: Nutley  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07110

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/062,368  
; FILING DATE: 19930514  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sias Ph.D., Stacey R.  
; REGISTRATION NUMBER: 32,630  
; REFERENCE/DOCKET NUMBER: 8584

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 814-2863  
; TELEFAX: (510) 814-2977  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 803 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-062-368-4

Query Match 75.0%; Score 30; DB 1; Length 803;  
Best Local Similarity 83.3%; Pred. No. 5.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|  
Db 705 YEHDAF 710

## RESULT 77

US-09-540-236-3443  
; Sequence 3443, Application US/09540236  
; Patent No. 6673910  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 3443  
; LENGTH: 816  
; TYPE: PRT  
; ORGANISM: M. catarrhalis  
US-09-540-236-3443

Query Match 75.0%; Score 30; DB 4; Length 816;  
Best Local Similarity 57.1%; Pred. No. 5.6e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|  
Db 797 YIEDAPI 803

## RESULT 78

US-08-354-685-4  
; Sequence 4, Application US/08354685  
; Patent No. 5498695  
; GENERAL INFORMATION:  
; APPLICANT: Daumy, Gaston O.  
; APPLICANT: Reiter, Lawrence A.  
; TITLE OF INVENTION: PARA-NITROANILIDE PEPTIDES  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dr. Peter C. Richardson  
; STREET: 235 East 42nd Street, 20th Floor  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10017-5755  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/354,685  
; FILING DATE:  
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 981,153  
; FILING DATE: 24-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Strassburger, Philip C.  
; REGISTRATION NUMBER: 34,258  
; REFERENCE/DOCKET NUMBER: PC8352  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)573-5731  
; TELEFAX: (212)573-1939  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-354-685-4

Query Match 72.5%; Score 29; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 YVHDA 5  
|||  
Db 1 YVHDA 5

RESULT 79  
US-09-902-540-14474  
; Sequence 14474, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 14474  
; LENGTH: 97  
; TYPE: PRT  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-14474

Query Match 72.5%; Score 29; DB 4; Length 97;  
Best Local Similarity 100.0%; Pred. No. 96; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 3 HDAPV 7  
|||  
Db 5 HDAPV 9

RESULT 80  
US-09-281-760E-36  
; Sequence 36, Application US/09281760E  
; Patent No. 6734287  
; GENERAL INFORMATION:  
; APPLICANT: Lawton, Robert  
; APPLICANT: Mermer, Brian  
; APPLICANT: Francoeur, Greg  
; TITLE OF INVENTION: Specific Binding Protein for Treating  
; TITLE OF INVENTION: Canine Allergy  
; FILE REFERENCE: 01-1275A  
; CURRENT APPLICATION NUMBER: US/09/281,760E  
; CURRENT FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: 09/058,331

; PRIOR FILING DATE: 1998-04-09  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (136)..(136)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (413)..(414)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (451)..(451)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (460)..(462)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (500)..(500)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (530)..(530)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (568)..(568)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (847)..(849)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (853)..(853)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1382)..(1382)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1832)..(1832)  
; OTHER INFORMATION: "n" stands for any nucleic acid  
US-09-281-760E-36

Query Match 72.5%; Score 29; DB 4; Length 107;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02; Indels 1; Gaps 0;  
Matches 5; Conservative 0; Mismatches 1;

QY 1 YVHDAP 6  
|||  
Db 19 YVHKAP 24

RESULT 81  
US-09-252-991A-23454  
; Sequence 23454, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18



; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23454  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23454

Query Match 72.5%; Score 29; DB 4; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDA 5  
|||  
Db 101 YVHDA 105

RESULT 82  
US-09-543-681A-5202  
; Sequence 5202, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 5202  
; LENGTH: 145  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-5202

Query Match 72.5%; Score 29; DB 4; Length 145;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHADPV 7  
|:|:|  
Db 136 YLHETPV 142

RESULT 83  
US-09-252-991A-20957  
; Sequence 20957, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20957  
; LENGTH: 178  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20957

Query Match 72.5%; Score 29; DB 4; Length 178;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 HDAPV 7  
|||||  
Db 166 HDAPV 170

RESULT 84  
US-09-107-532A-7290  
; Sequence 7290, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneka  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 7290:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 179 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8) LOCATION 1...179  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7290:

Query Match 72.5%; Score 29; DB 4; Length 179;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAPV 7  
|||||  
Db 72 HDAPV 76

RESULT 85  
US-09-252-991A-19320  
; Sequence 19320, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; PRIOR FILING DATE: 1999-02-18  
;; CURRENT APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 19320  
;; TYPE: PRT  
;; LENGTH: 183  
;; ORGANISM: Pseudomonas aeruginosa  
;; FEATURE:  
;; NAME/KEY: UNSURE  
;; LOCATION: (163), (164), (167), (169), (170), (171)  
;; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.  
US-09-252-991A-19320

Query Match 72.5%; Score 29; DB 4; Length 183;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 VHDAP 6  
|||  
Db 174 VHDAP 178

RESULT 86  
US-09-949-016-7376  
; Sequence 7376, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7376  
; LENGTH: 205  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7376

Query Match 72.5%; Score 29; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 VHDAP 6  
|||  
Db 190 VHDAP 194

RESULT 87  
US-08-417-822A-2  
; Sequence 2, Application US/08417822A  
; Patent No. 5639454  
; GENERAL INFORMATION:  
; APPLICANT: Suzanne M. Thiem  
; TITLE OF INVENTION: Recombinant Baculovirus  
; WITH Broad Host Range  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Ian C. McLeod  
;; STREET: 2190 Commons Parkway  
;; CITY: Okemos  
;; STATE: Michigan  
;; COUNTRY: USA  
;; ZIP: 48864  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
;; MEDIUM TYPE: storage  
;; COMPUTER: Acer  
;; OPERATING SYSTEM: MS-DOS 5.00  
;; SOFTWARE: Wordperfect 5.1  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/417,822A  
;; FILING DATE: April 6, 1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ian C. McLeod  
;; REGISTRATION NUMBER: 20,931  
;; REFERENCE/DOCKET NUMBER: MSU 4.1-241  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (517) 347-4100  
;; TELEFAX: (517) 347-4103  
;; TELEX: No. 5639454e  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 218  
;; TYPE: Amino Acid  
;; STRANDEDNESS: Single  
;; TOPOLOGY: Linear  
;; MOLECULE TYPE: DNA  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: No  
;; FRAGMENT TYPE:  
;; ORIGINAL SOURCE:  
;; ORGANISM: Lymantria dispar  
;; STRAIN: N/A  
;; INDIVIDUAL ISOLATE: N/A  
;; DEVELOPMENTAL STAGE: N/A  
;; HAPLOTYPE: N/A  
;; TISSUE TYPE: N/A  
;; CELL TYPE: N/A  
;; CELL LINE: N/A  
;; ORGANELLE: N/A  
;; IMMEDIATE SOURCE: N/A  
;; POSITION IN GENOME: N/A  
;; FEATURE:  
;; NAME/KEY: protein encoded by DNA  
;; LOCATION:  
;; IDENTIFICATION METHOD: sequencing  
;; OTHER INFORMATION: protein  
;; OTHER INFORMATION: for increasing host  
;; OTHER INFORMATION: range encoded by SEQ ID NO:1  
;; PUBLICATION INFORMATION:  
US-08-417-822A-2

Query Match 72.5%; Score 29; DB 1; Length 218;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 YVHDAPV 7  
|||  
Db 108 YAHGDFL 114

RESULT 88  
US-09-252-991A-28448  
; Sequence 28448, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252.991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 28448  
LENGTH: 242  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-28448

Query Match 72.5%; Score 29; DB 4; Length 242;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAPV 7  
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Db 79 HDAPV 83

RESULT 89  
US-09-489-039A-9197  
Sequence 9197, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 9197  
LENGTH: 245  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9197

Query Match 72.5%; Score 29; DB 4; Length 245;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
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Db 86 VHDAP 90

RESULT 90  
US-09-489-039A-7881  
Sequence 7881, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 7881  
LENGTH: 254  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae

US-09-489-039A-7881

Query Match 72.5%; Score 29; DB 4; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAPV 7  
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Db 84 HDAPV 88

RESULT 91  
US-09-724-797-12  
Sequence 12, Application US/09724797  
Patent No. 6733998  
GENERAL INFORMATION:  
APPLICANT: Jon S. THORSON  
TITLE OF INVENTION: MICROMONOSPORA ECHINOSPORA GENES  
TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF  
TITLE OF INVENTION: CALICHEAMICIN AND SELF-RESISTANCE THERETO  
FILE REFERENCE: 2653-40  
CURRENT APPLICATION NUMBER: US/09/724,797  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 60/111,325  
PRIOR FILING DATE: 1998-12-07  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 263  
TYPE: PRT  
ORGANISM: Bacteria  
US-09-724-797-12

Query Match 72.5%; Score 29; DB 4; Length 263;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
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Db 18 FVHDSP 23

RESULT 92  
US-09-489-039A-13000  
Sequence 13000, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 13000  
LENGTH: 274  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13000

Query Match 72.5%; Score 29; DB 4; Length 274;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAPV 7  
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Db 127 HDAPV 131

RESULT 93  
US-09-248-796A-17294

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; Sequence 17294, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17294
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17294

Query Match      72.5%; Score 29; DB 4; Length 289;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      208 YVIDAPV 214

RESULT 94
US-09-270-767-33591
; Sequence 33591, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33591
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33591

Query Match      72.5%; Score 29; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDA 5
Db      220 YVHDA 224

RESULT 95
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURE:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel.
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2

Query Match      72.5%; Score 29; DB 4; Length 312;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAP 6
Db      124 YVHKAP 129

RESULT 96
US-09-270-767-58348
; Sequence 58348, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58348
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-58348

Query Match      72.5%; Score 29; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 HDAPV 7
Db      28 HDAPV 32

RESULT 97
US-09-252-991A-33007
; Sequence 33007, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33007
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33007
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Query Match 72.5%; Score 29; DB 4; Length 345;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
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QY 3 HDAVP 7  
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Db 22 HDAVP 26

RESULT 98  
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; Sequence 7606, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7606  
; LENGTH: 349  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-7606

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Best Local Similarity 71.4%; Pred. No. 3.7e+02;  
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QY 1 YVHDAPV 7  
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Db 232 YVGDAPI 238

RESULT 99  
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; Sequence 6524, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 6524  
; LENGTH: 354  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-6524

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Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAVP 7  
|||||  
Db 38 HDAVP 42

RESULT 100  
US-09-538-092-1226  
; Sequence 1226, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.

; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542  
; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CurapatSeqFormatter Version 0.9  
; SEQ ID NO 1226  
; LENGTH: 368  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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; NAME/KEY: misc feature  
; LOCATION: (0)..(0)  
; OTHER INFORMATION: Polypeptide Accession Number P78406  
US-09-538-092-1226

Query Match 72.5%; Score 29; DB 4; Length 368;  
Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAVP 7  
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Db 126 HDAVP 130

Search completed: June 30, 2005, 22:33:02  
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OM protein - protein search, using sw model

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Title: US-09-874-350C-210

Perfect score: 40

Sequence: 1 YVHDAPV 7

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#### SUMMARIES

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					Sequence 216, App
					Sequence 217, App
					Sequence 200, App
					Sequence 88, Appl
					Sequence 89, Appl
					Sequence 90, Appl
					Sequence 55, Appl
					Sequence 56, Appl
					Sequence 57, Appl
					Sequence 218, App

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14	40	100.0	16	10	US-09-747-287-92	Sequence 92, Appl
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17	40	100.0	16	10	US-09-747-287-206	Sequence 206, App
18	40	100.0	16	11	US-09-874-350A-58	Sequence 58, Appl
19	40	100.0	16	11	US-09-874-350A-59	Sequence 59, Appl
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27	40	100.0	17	11	US-09-874-350A-65	Sequence 65, Appl
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58	40	100.0	269	17	US-10-491-997-84	Sequence 84, Appl
59	37	92.5	67	16	US-10-437-963-178722	Sequence 178722, Sequence 207, App
60	36	90.0	14	10	US-09-747-287-207	Sequence 4, Appl
61	36	90.0	20	9	US-09-780-575-4	Sequence 127296, Sequence 132031,
62	36	90.0	1566	16	US-10-437-963-127296	Sequence 172, App
63	34	85.0	156	16	US-10-437-963-132031	Sequence 99, Appl
64	33	82.5	16	11	US-09-874-350A-172	Sequence 229242, Sequence 274088,
65	33	82.5	18	10	US-09-747-287-99	Sequence 247918,
66	33	82.5	58	16	US-10-425-115-229242	Sequence 3074, Ap
67	33	82.5	78	16	US-10-425-115-274088	Sequence 56, Appl
68	33	82.5	120	16	US-10-425-115-247918	Sequence 110, App
69	33	82.5	272	15	US-10-320-797-3074	Sequence 152111,
70	33	82.5	419	15	US-10-275-026A-56	Sequence 21825, A
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72	32	80.0	45	16	US-10-437-963-152111	Sequence 19932,
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## ALIGNMENTS

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Sequence 189250,
Sequence 272422, A
Sequence 47269, A
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Sequence 9926, Ap
Sequence 125228,
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Sequence 59691, A
Sequence 263, App
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Sequence 10285, A
Sequence 2, Appli
Sequence 9, Appli
Sequence 31385,
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Sequence 234254,
Sequence 78128, A
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Sequence 51014, A
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Sequence 321366,
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Sequence 13313, A
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Sequence 516, App
Sequence 57691, A
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Sequence 323, App
Sequence 356, App
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Sequence 46232, A
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Sequence 13098, A
Sequence 13105, A
Sequence 18870, A
Sequence 19169,
Sequence 7931, Ap
Sequence 250438,
Sequence 19778, A
Sequence 22131, A
Sequence 131062,
Sequence 154712,
Sequence 64, Appl
Sequence 64, Appl
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Query Match 100.0%; Score 40; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAVP 7  
Db 1 YVHDAVP 7  
|||||

RESULT 2  
US-09-874-350A-216  
Sequence 216, Application US/09874350A  
Publication No. US20040096926A1  
GENERAL INFORMATION:  
APPLICANT: Oncoimmunin, Inc.  
APPLICANT: Komoriya, Akira  
APPLICANT: Packard, Beverly  
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S  
FILE REFERENCE: 300-903840US  
CURRENT APPLICATION NUMBER: US/09/874,350A  
CURRENT FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: PCT/US98/00300  
PRIOR FILING DATE: 1998-02-20  
PRIOR APPLICATION NUMBER: PCT/US00/24882  
PRIOR FILING DATE: 2000-09-11  
PRIOR APPLICATION NUMBER: US 09/394,019  
PRIOR FILING DATE: 1999-09-10  
PRIOR APPLICATION NUMBER: US 08/802,981  
PRIOR FILING DATE: 1997-02-20  
NUMBER OF SEQ ID NOS: 221  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 216  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide substrate  
NAME/KEY: Artificial  
LOCATION: (1)..(7)  
OTHER INFORMATION: Artificial protease substrate  
US-09-874-350A-210



Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 1 YVHDAPV 7

## RESULT 3

US-09-874-350A-217  
; Sequence 217, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:

; APPLICANT: Oncolimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES  
; TITLE OF INVENTION: AND METHODS OF USE THEREOF  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 217  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: Y is "D" form amino acid  
US-09-874-350A-217

Query Match 100.0%; Score 40; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 1 YVHDAPV 7

## RESULT 4

US-09-572-404B-200  
; Sequence 200, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 200  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in IL1A at 112-121 and may interact with Sequenc  
; OTHER INFORMATION: in this patent.  
US-09-572-404B-200

Query Match 100.0%; Score 40; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 2 YVHDAPV 8

## RESULT 5

US-09-747-287-88  
; Sequence 88, Application US/09747287  
; Publication No. US20030207264A1  
; GENERAL INFORMATION:

; APPLICANT: KOMORIYA, AKIRA  
; APPLICANT: PACKARD, BEVERLY S.  
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES  
; FILE REFERENCE: 300-948600US  
; CURRENT APPLICATION NUMBER: US/09/747,287  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/349,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 242  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 88  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide.  
US-09-747-287-88

Query Match 100.0%; Score 40; DB 10; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 4 YVHDAPV 10

## RESULT 6

US-09-747-287-89  
; Sequence 89, Application US/09747287  
; Publication No. US20030207264A1  
; GENERAL INFORMATION:

; APPLICANT: KOMORIYA, AKIRA  
; APPLICANT: PACKARD, BEVERLY S.  
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES  
; FILE REFERENCE: 300-948600US  
; CURRENT APPLICATION NUMBER: US/09/747,287  
; CURRENT FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/349,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 242  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 89  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide.  
US-09-747-287-89

```
Query Match      100.0%; Score 40; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.33; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 YVHDAVP 7
        |||||
Db       4 YVHDAVP 10

RESULT 7
US-09-747-287-90
; Sequence 90, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
US-09-747-287-90

Query Match      100.0%; Score 40; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.33; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 YVHDAVP 7
        |||||
Db       4 YVHDAVP 10

RESULT 8
US-09-874-350A-55
; Sequence 55, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
US-09-874-350A-55

Query Match      100.0%; Score 40; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.33; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 YVHDAVP 7
        |||||
Db       4 YVHDAVP 10

RESULT 9
US-09-874-350A-56
; Sequence 56, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
US-09-874-350A-56

Query Match      100.0%; Score 40; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.33; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 YVHDAVP 7
        |||||
Db       4 YVHDAVP 10

RESULT 10
US-09-874-350A-57
; Sequence 57, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
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;; PRIOR FILING DATE: 1998-02-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/24882  
;; PRIOR FILING DATE: 2000-09-11  
;; PRIOR APPLICATION NUMBER: US 09/394,019  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US 08/802,981  
;; PRIOR FILING DATE: 1997-02-20  
;; NUMBER OF SEQ ID NOS: 221  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 57  
;; LENGTH: 14  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Protease indicator  
;; NAME/KEY: misc feature  
;; LOCATION: (3)..(3)  
;; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid  
US-09-874-350A-57

Query Match 100.0%; Score 40; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 4 YVHDAPV 10  
|||||

## RESULT 11

US-09-874-350A-218  
;; Sequence 218, Application US/09874350A  
;; Publication No. US20040096926A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Oncoimmunin, Inc.  
;; APPLICANT: Komoriya, Akira  
;; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES  
;; FILE REFERENCE: 300-903840US  
;; CURRENT APPLICATION NUMBER: US/09/874,350A  
;; CURRENT FILING DATE: 2001-06-04  
;; PRIOR APPLICATION NUMBER: PCT/US98/00300  
;; PRIOR FILING DATE: 1998-02-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/24882  
;; PRIOR FILING DATE: 2000-09-11  
;; PRIOR APPLICATION NUMBER: US 09/394,019  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US 08/802,981  
;; NUMBER OF SEQ ID NOS: 221  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 218  
;; LENGTH: 14  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Protease indicator  
US-09-874-350A-218

Query Match 100.0%; Score 40; DB 11; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 4 YVHDAPV 10  
|||||

## RESULT 12

US-09-874-350A-213  
;; Sequence 213, Application US/09874350A  
;; Publication No. US20040096926A1

;; GENERAL INFORMATION:  
;; APPLICANT: Oncoimmunin, Inc.  
;; APPLICANT: Komoriya, Akira  
;; APPLICANT: Packard, Beverly  
;; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES  
;; FILE REFERENCE: 300-903840US  
;; CURRENT APPLICATION NUMBER: US/09/874,350A  
;; CURRENT FILING DATE: 2001-06-04  
;; PRIOR APPLICATION NUMBER: PCT/US98/00300  
;; PRIOR FILING DATE: 1998-02-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/24882  
;; PRIOR FILING DATE: 2000-09-11  
;; PRIOR APPLICATION NUMBER: US 09/394,019  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US 08/802,981  
;; PRIOR FILING DATE: 1997-02-20  
;; NUMBER OF SEQ ID NOS: 221  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 213  
;; LENGTH: 15  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic peptide substrate  
;; NAME/KEY: MOD RES  
;; LOCATION: (1)..(1)  
;; OTHER INFORMATION: K is blocked with Fmoc  
;; NAME/KEY: MOD RES  
;; LOCATION: (4)..(4)  
;; OTHER INFORMATION: X is epsilon-aminocaproic acid  
;; NAME/KEY: MOD RES  
;; LOCATION: (14)..(14)  
;; OTHER INFORMATION: X is epsilon-aminocaproic acid  
;; NAME/KEY: MOD RES  
;; LOCATION: (15)..(15)  
;; OTHER INFORMATION: K is blocked with amide  
US-09-874-350A-213

Query Match 100.0%; Score 40; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 6 YVHDAPV 12  
|||||

## RESULT 13

US-09-747-287-91  
;; Sequence 91, Application US/09747287  
;; Publication No. US20030207264A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KOMORIYA, AKIRA  
;; APPLICANT: PACKARD, BEVERLY S.  
;; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL SAMPLES  
;; FILE REFERENCE: 300-948600US  
;; CURRENT APPLICATION NUMBER: US/09/747,287  
;; CURRENT FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: US 09/349,019  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US08/802,981  
;; PRIOR FILING DATE: 1997-02-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/24882  
;; PRIOR FILING DATE: 2000-09-11  
;; NUMBER OF SEQ ID NOS: 242  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 91  
;; LENGTH: 16  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:

```
; OTHER INFORMATION: Synthetic peptide.
US-09-747-287-91

Query Match      100.0%; Score 40; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 5 YVHDAVP 11

RESULT 14
US-09-747-287-92
; Sequence 92, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
US-09-747-287-92

Query Match      100.0%; Score 40; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 5 YVHDAVP 11

RESULT 15
US-09-747-287-93
; Sequence 93, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial

; OTHER INFORMATION: Synthetic peptide.
US-09-747-287-93

Query Match      100.0%; Score 40; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 6 YVHDAVP 12

RESULT 17
US-09-747-287-206
; Sequence 206, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242

; OTHER INFORMATION: Synthetic peptide.
US-09-747-287-205

Query Match      100.0%; Score 40; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
Db 6 YVHDAVP 12

RESULT 17
US-09-747-287-206
; Sequence 206, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242

; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-747-287-205
```

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 206

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic peptide.

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (4)..(4)

; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (12)..(12)

; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid

; US-09-747-287-206

Query Match 100.0%; Score 40; DB 10; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.38; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7

Db 4 YVHDAPV 10

RESULT 18

US-09-874-350A-58

; Sequence 58, Application US/09874350A

; Publication No. US20040096926A1

; GENERAL INFORMATION:

; APPLICANT: Oncoimmunin, Inc.

; APPLICANT: Komoriya, Akira

; APPLICANT: Packard, Beverly

; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL

; FILE OF INVENTION: AND METHODS OF USE THEREOF

; FILE REFERENCE: 300-903840US

; CURRENT APPLICATION NUMBER: US/09/874,350A

; CURRENT FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: PCT/US98/00300

; PRIOR FILING DATE: 1998-02-20

; PRIOR APPLICATION NUMBER: PCT/US00/24882

; PRIOR FILING DATE: 2000-09-11

; PRIOR APPLICATION NUMBER: US 09/394,019

; PRIOR FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: US 08/802,981

; PRIOR FILING DATE: 1997-02-20

; NUMBER OF SEQ ID NOS: 221

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 58

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Protease indicator

; NAME/KEY: misc\_feature

; LOCATION: (3)..(3)

; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

; US-09-874-350A-58

Query Match 100.0%; Score 40; DB 11; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7

Db 5 YVHDAPV 11

RESULT 19

US-09-874-350A-59

; Sequence 59, Application US/09874350A

; Publication No. US20040096926A1

; GENERAL INFORMATION:

; APPLICANT: Oncoimmunin, Inc.

; APPLICANT: Komoriya, Akira

; APPLICANT: Packard, Beverly

; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL

; FILE OF INVENTION: AND METHODS OF USE THEREOF

; FILE REFERENCE: 300-903840US

; CURRENT APPLICATION NUMBER: US/09/874,350A

; CURRENT FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: PCT/US98/00300

; PRIOR FILING DATE: 1998-02-20

; PRIOR APPLICATION NUMBER: PCT/US00/24882

; PRIOR FILING DATE: 2000-09-11

; PRIOR APPLICATION NUMBER: US 09/394,019

; PRIOR FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: US 08/802,981

; PRIOR FILING DATE: 1997-02-20

; NUMBER OF SEQ ID NOS: 221

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 59

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Protease indicator

; NAME/KEY: misc\_feature

; LOCATION: (3)..(3)

; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

; US-09-874-350A-59

Query Match 100.0%; Score 40; DB 11; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.38;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7

Db 5 YVHDAPV 11

RESULT 20

US-09-874-350A-60

; Sequence 60, Application US/09874350A

; Publication No. US20040096926A1

; GENERAL INFORMATION:

; APPLICANT: Oncoimmunin, Inc.

; APPLICANT: Komoriya, Akira

; APPLICANT: Packard, Beverly

; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL

; FILE OF INVENTION: AND METHODS OF USE THEREOF

; FILE REFERENCE: 300-903840US

; CURRENT APPLICATION NUMBER: US/09/874,350A

; CURRENT FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: PCT/US98/00300

; PRIOR FILING DATE: 1998-02-20

; PRIOR APPLICATION NUMBER: PCT/US00/24882

; PRIOR FILING DATE: 2000-09-11

; PRIOR APPLICATION NUMBER: US 09/394,019

; PRIOR FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: US 08/802,981

; PRIOR FILING DATE: 1997-02-20

; NUMBER OF SEQ ID NOS: 221

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 60

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Protease indicator

; NAME/KEY: misc\_feature

; LOCATION: (3)..(3)

; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid

; US-09-874-350A-60

```
Query Match      100.0%; Score 40; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 YVHDAPV 7
Db      5 YVHDAPV 11

RESULT 21
US-09-874-350A-214
; Sequence 214, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncommunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 214
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: K is blocked with Fmoc
; NAME/KEY: MOD RES
; LOCATION: (6)..(6)
; OTHER INFORMATION: X is D form tetrahydroisoquinoline-3-carboxylic acid
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is episilon-aminocaproic acid
; NAME/KEY: MOD RES
; LOCATION: (15)..(15)
; OTHER INFORMATION: X is episilon-aminocaproic acid
;
US-09-874-350A-214

Query Match      100.0%; Score 40; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 YVHDAPV 7
Db      4 YVHDAPV 10

RESULT 22
US-09-874-350A-219
; Sequence 219, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncommunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
```

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; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 219
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
;
US-09-874-350A-219

Query Match      100.0%; Score 40; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.38; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 YVHDAPV 7
Db      5 YVHDAPV 11

RESULT 23
US-09-874-350A-61
; Sequence 61, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncommunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
; NAME/KEY: misc.feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
; NAME/KEY: misc.feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
;
US-09-874-350A-61

Query Match      100.0%; Score 40; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.4; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 YVHDAPV 7
Db      6 YVHDAPV 12
```

RESULT 24  
US-09-874-350A-62  
; Sequence 62, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 62  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Protease indicator  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid  
; NAME/KEY: misc feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid  
US-09-874-350A-62

Query Match 100.0%; Score 40; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
DB 6 YVHDAPV 12

RESULT 25  
US-09-874-350A-63  
; Sequence 63, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 63  
; LENGTH: 17  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Protease indicator  
; NAME/KEY: misc feature  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid  
; NAME/KEY: misc feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid  
US-09-874-350A-63

Query Match 100.0%; Score 40; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
DB 6 YVHDAPV 12

RESULT 26  
US-09-874-350A-64  
; Sequence 64, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 64  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Protease indicator  
; NAME/KEY: misc feature  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid  
; NAME/KEY: misc feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid  
US-09-874-350A-64

Query Match 100.0%; Score 40; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
DB 6 YVHDAPV 12

RESULT 27  
US-09-874-350A-65  
; Sequence 65, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 64  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Protease indicator  
; NAME/KEY: misc feature  
; LOCATION: (3)..(3)  
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid  
; NAME/KEY: misc feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid  
US-09-874-350A-64

Query Match 100.0%; Score 40; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.4;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
DB 6 YVHDAPV 12

RESULT 27  
US-09-874-350A-65  
; Sequence 65, Application US/09874350A  
; Publication No. US20040096926A1  
; GENERAL INFORMATION:  
; APPLICANT: Oncoimmunin, Inc.  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly  
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL  
; FILE REFERENCE: 300-903840US  
; CURRENT APPLICATION NUMBER: US/09/874,350A  
; CURRENT FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: PCT/US98/00300  
; PRIOR FILING DATE: 1998-02-20  
; PRIOR APPLICATION NUMBER: PCT/US00/24882  
; PRIOR FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: US 09/394,019  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 08/802,981  
; PRIOR FILING DATE: 1997-02-20  
; NUMBER OF SEQ ID NOS: 221  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 63  
; LENGTH: 17  
; TYPE: PRT

```
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-9038400S
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
; NAME/KEY: misc feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
; US-09-874-350A-65

Query Match          100.0%; Score 40; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.4; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
        |||||
Db      6 YVHDAPV 12

RESULT 28
US-09-747-287-94
; Sequence 94, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
; US-09-747-287-95

Query Match          100.0%; Score 40; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
        |||||
Db      6 YVHDAPV 12

RESULT 30
US-09-747-287-96
; Sequence 96, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
```

```
US-09-747-287-94
Query Match          100.0%; Score 40; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
        |||||
Db      6 YVHDAPV 12

RESULT 29
US-09-747-287-95
; Sequence 95, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 95
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
; US-09-747-287-95

Query Match          100.0%; Score 40; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
        |||||
Db      6 YVHDAPV 12

RESULT 30
US-09-747-287-96
; Sequence 96, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; FILE REFERENCE: 300-948600US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 95
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
```



;; PRIOR FILING DATE: 2000-09-11  
;; NUMBER OF SEQ ID NOS: 242  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 96  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic peptide.  
;;  
;; NAME/KEY: misc feature  
;; LOCATION: (4)..(4)  
;; OTHER INFORMATION: Xaa is epilson-aminocaproic acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (14)..(14)  
;; OTHER INFORMATION: Xaa is epilson-aminocaproic acid  
US-09-747-287-96

Query Match 100.0%; Score 40; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
| | | | |  
Db 6 YVHDAVP 12

RESULT 31  
US-09-747-287-97  
;; Sequence 97, Application US/09747287  
;; Publication No. US20030207264A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KOMORIYA, AKIRA  
;; APPLICANT: PACKARD, BEVERLY S.  
;; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
;; FILE REFERENCE: 300-948600US  
;; CURRENT APPLICATION NUMBER: US/09/747,287  
;; CURRENT FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: US 09/349,019  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US08/802,981  
;; PRIOR FILING DATE: 1997-02-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/24882  
;; PRIOR FILING DATE: 2000-09-11  
;; NUMBER OF SEQ ID NOS: 242  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 97  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic peptide.  
;;  
;; NAME/KEY: misc feature  
;; LOCATION: (4)..(4)  
;; OTHER INFORMATION: Xaa is epilson-aminocaproic acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (14)..(14)  
;; OTHER INFORMATION: Xaa is epilson-aminocaproic acid  
US-09-747-287-97

Query Match 100.0%; Score 40; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
| | | | |  
Db 6 YVHDAVP 12

RESULT 32  
US-09-747-287-98  
;; Sequence 98, Application US/09747287  
;; Publication No. US20030207264A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KOMORIYA, AKIRA  
;; APPLICANT: PACKARD, BEVERLY S.  
;; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
;; FILE REFERENCE: 300-948600US  
;; CURRENT APPLICATION NUMBER: US/09/747,287  
;; CURRENT FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: US 09/349,019  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US08/802,981  
;; PRIOR FILING DATE: 1997-02-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/24882  
;; PRIOR FILING DATE: 2000-09-11  
;; NUMBER OF SEQ ID NOS: 242  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 98  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic peptide.  
;;  
;; NAME/KEY: misc feature  
;; LOCATION: (4)..(4)  
;; OTHER INFORMATION: Xaa is epilson-aminocaproic acid  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (14)..(14)  
;; OTHER INFORMATION: Xaa is epilson-aminocaproic acid  
US-09-747-287-98

Query Match 100.0%; Score 40; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
| | | | |  
Db 6 YVHDAVP 12

RESULT 33  
US-09-747-287-204  
;; Sequence 204, Application US/09747287  
;; Publication No. US20030207264A1  
;; GENERAL INFORMATION:  
;; APPLICANT: KOMORIYA, AKIRA  
;; APPLICANT: PACKARD, BEVERLY S.  
;; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME  
;; FILE REFERENCE: 300-948600US  
;; CURRENT APPLICATION NUMBER: US/09/747,287  
;; CURRENT FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: US 09/349,019  
;; PRIOR FILING DATE: 1999-09-10  
;; PRIOR APPLICATION NUMBER: US08/802,981  
;; PRIOR FILING DATE: 1997-02-20  
;; PRIOR APPLICATION NUMBER: PCT/US00/24882  
;; PRIOR FILING DATE: 2000-09-11  
;; NUMBER OF SEQ ID NOS: 242  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 204  
;; LENGTH: 18  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic peptide.  
;;  
;; NAME/KEY: misc feature  
US-09-747-287-97

```
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-747-287-204

Query Match      100.0%; Score 40; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 6 YVHDAPV 12

RESULT 34
US-09-874-350A-66
; Sequence 66, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: Xaa is alpha-aminoisobutyric acid
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-874-350A-66

Query Match      100.0%; Score 40; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 7 YVHDAPV 13

RESULT 35
US-09-874-350A-170
; Sequence 170, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
```

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; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 170
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid (Ahx)
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid (Ahx)
US-09-874-350A-170

Query Match      100.0%; Score 40; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 6 YVHDAPV 12

RESULT 36
US-09-874-350A-171
; Sequence 171, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 171
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid (Ahx)
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid (Ahx)
US-09-874-350A-171
```

```
Query Match      100.0%; Score 40; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
    |||||
Db 6 YVHDAPV 12

RESULT 37
US-09-874-350A-212
; Sequence 212, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 212
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: K is blocked with Fmoc
; NAME/KEY: MOD RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is epsilon-aminocaproic acid
US-09-874-350A-212

Query Match      100.0%; Score 40; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
    |||||
Db 6 YVHDAPV 12

RESULT 38
US-09-874-350A-220
; Sequence 220, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
```

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; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 220
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-874-350A-220

Query Match      100.0%; Score 40; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
    |||||
Db 6 YVHDAPV 12

RESULT 39
US-09-874-350A-221
; Sequence 221, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 221
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Protease indicator
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
; NAME/KEY: misc feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: Y is "D" form amino acid
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-874-350A-221

Query Match      100.0%; Score 40; DB 11; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.43;
```

```
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
    |||||
Db 6 YVHDAVP 12

RESULT 40
US-10-716-029-198
; Sequence 198, Application US/10716029
; Publication No. US20040171038A1
; GENERAL INFORMATION:
; APPLICANT: Nicklin, Martin
; APPLICANT: Duff, Gordon
; APPLICANT: Kornman, Kenneth
; APPLICANT: Kolpin, Maryam R
; APPLICANT: Hsieh, Chung-Ming
; APPLICANT: Govindaraju, Raju
; APPLICANT: Aziz, Nazneen
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms
; TITLE OF INVENTION: The IL-1 Gene Cluster and Associated Inflammatory Polymorphisms
; FILE REFERENCE: 24299-524 CON
; CURRENT APPLICATION NUMBER: US/10/716,029
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/351,702
; PRIOR FILING DATE: 2003-01-25
; PRIOR APPLICATION NUMBER: 60/351,951
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 277
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 198
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-716-029-198

Query Match 100.0%; Score 40; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
    |||||
Db 12 YVHDAVP 18

RESULT 41
US-10-637-313-78
; Sequence 78, Application US/10637313
; Publication No. US20040229779A1
; GENERAL INFORMATION:
; APPLICANT: Ramesh Kekuda
; APPLICANT: Uriel Malyankar
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Sasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Stacie Casman
; APPLICANT: Ferenc Boldog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khramtsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patturajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
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; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 78
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-637-313-78

Query Match 100.0%; Score 40; DB 16; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
    |||||
Db 79 YVHDAVP 85

RESULT 42
US-10-637-313-84
; Sequence 84, Application US/10637313
; Publication No. US20040229779A1
; GENERAL INFORMATION:
; APPLICANT: Ramesh Kekuda
; APPLICANT: Uriel Malyankar
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Sasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Stacie Casman
; APPLICANT: Ferenc Boldog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khramtsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patturajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/301550
```

; PRIOR FILING DATE: 2001-06-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 255  
; SOFTWARE: CuraseqList version 0.1

; SEQ ID NO 84  
; LENGTH: 219

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-637-313-84

Query Match 100.0%; Score 40; DB 16; Length 219;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7

Db 79 YVHDAPV 85

RESULT 43

US-10-637-313-86

; Sequence 86, Application US/10637313  
; Publication No. US20040229779A1

; GENERAL INFORMATION:

; APPLICANT: Ramesh Kekuda

; APPLICANT: Uriel Malyankar

; APPLICANT: Li Li

; APPLICANT: David Anderson

; APPLICANT: Sasha Guo

; APPLICANT: Mei Zhong

; APPLICANT: Muralidhara Padigar

; APPLICANT: Stacie Casman

; APPLICANT: Ferenc Boldog

; APPLICANT: Charles Miller

; APPLICANT: Nikolai Khrantsov

; APPLICANT: Corine Vernet

; APPLICANT: Meera Patturajan

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-593B

; CURRENT APPLICATION NUMBER: US/10/637,313

; CURRENT FILING DATE: 2003-08-08

; PRIOR APPLICATION NUMBER: 10/162335

; PRIOR FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: 60/295607

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/295661

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/296404

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296418

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/298285

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/298556

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/299949

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: 60/300883

; PRIOR FILING DATE: 2001-06-26

; PRIOR APPLICATION NUMBER: 60/301550

; PRIOR FILING DATE: 2001-06-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 255

; SOFTWARE: CuraseqList version 0.1

; SEQ ID NO 85

; LENGTH: 219

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-637-313-86

Query Match 100.0%; Score 40; DB 16; Length 219;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7

Db 79 YVHDAPV 85

RESULT 44

US-10-637-313-88

; Sequence 88, Application US/10637313  
; Publication No. US20040229779A1

; GENERAL INFORMATION:

; APPLICANT: Ramesh Kekuda

; APPLICANT: Uriel Malyankar

; APPLICANT: Li Li

; APPLICANT: David Anderson

; APPLICANT: Sasha Guo

; APPLICANT: Mei Zhong

; APPLICANT: Muralidhara Padigar

; APPLICANT: Stacie Casman

; APPLICANT: Ferenc Boldog

; APPLICANT: Charles Miller

; APPLICANT: Nikolai Khrantsov

; APPLICANT: Corine Vernet

; APPLICANT: Meera Patturajan

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

; FILE REFERENCE: 21402-593B

; CURRENT APPLICATION NUMBER: US/10/637,313

; CURRENT FILING DATE: 2003-08-08

; PRIOR APPLICATION NUMBER: 10/162335

; PRIOR FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: 60/295607

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/295661

; PRIOR FILING DATE: 2001-06-04

; PRIOR APPLICATION NUMBER: 60/296404

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/296418

; PRIOR FILING DATE: 2001-06-06

; PRIOR APPLICATION NUMBER: 60/298285

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: 60/298556

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/299949

; PRIOR FILING DATE: 2001-06-21

; PRIOR APPLICATION NUMBER: 60/300883

; PRIOR FILING DATE: 2001-06-26

; PRIOR APPLICATION NUMBER: 60/301550

; PRIOR FILING DATE: 2001-06-28

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 255

; SOFTWARE: CuraseqList version 0.1

; SEQ ID NO 88

; LENGTH: 219

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-637-313-88

Query Match 100.0%; Score 40; DB 16; Length 219;  
Best Local Similarity 100.0%; Pred. No. 5.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7

Db 79 YVHDAPV 85

RESULT 45

US-10-637-313-90

; Sequence 90, Application US/10637313

; Publication No. US20040229779A1

; GENERAL INFORMATION:

; APPLICANT: Ramesh Kekuda

; APPLICANT: Uriel Malyankar

```
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Sasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Stacie Casman
; APPLICANT: Ferenc Boldog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khrantsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patturajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 90
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-637-313-90

Query Match 100.0%; Score 40; DB 16; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 79 YVHDAPV 85

RESULT 46
US-10-637-313-92
; Sequence 92, Application US/10637313
; Publication No. US20040229779A1
; GENERAL INFORMATION:
; APPLICANT: Ramesh Kekuda
; APPLICANT: Uriel Malyankar
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Sasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Stacie Casman
; APPLICANT: Ferenc Boldog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khrantsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patturajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
```

```
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/298285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 92
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-637-313-92

Query Match 100.0%; Score 40; DB 16; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 79 YVHDAPV 85

RESULT 47
US-10-637-313-94
; Sequence 94, Application US/10637313
; Publication No. US20040229779A1
; GENERAL INFORMATION:
; APPLICANT: Ramesh Kekuda
; APPLICANT: Uriel Malyankar
; APPLICANT: Li Li
; APPLICANT: David Anderson
; APPLICANT: Sasha Guo
; APPLICANT: Mei Zhong
; APPLICANT: Muralidhara Padigaru
; APPLICANT: Stacie Casman
; APPLICANT: Ferenc Boldog
; APPLICANT: Charles Miller
; APPLICANT: Nikolai Khrantsov
; APPLICANT: Corine Vernet
; APPLICANT: Meera Patturajan
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
; CURRENT APPLICATION NUMBER: US/10/637,313
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 10/162335
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296418
; PRIOR FILING DATE: 2001-06-06
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-593B
```

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;
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300883
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/301550
; PRIOR FILING DATE: 2001-06-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 94
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-637-313-94

Query Match          100.0%; Score 40; DB 16; Length 219;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAV 7
Db      79 YVHDAV 85

RESULT 48
US-09-840-707A-2
; Sequence 2, Application US/09840707A
; Patent No. US20020077276A1
; GENERAL INFORMATION:
; APPLICANT: Ignatjev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INJECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Interleukin-1 beta (catabolin)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: P01584/Genbank
; DATABASE ENTRY DATE: 2001-08-20
US-09-840-707A-2

Query Match          100.0%; Score 40; DB 9; Length 269;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAV 7
Db      113 YVHDAV 119

RESULT 49
US-09-770-528-10
; Sequence 10, Application US/09770528
; Patent No. US20020164332A1
; GENERAL INFORMATION:
; APPLICANT: Hedrick, Joseph A.
; Sana, Theodore R.
; Bazan, Fernando J.
```

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;
; Kastelein, Robert A.
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
; and Methods
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,528
; FILING DATE: 25-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/130,972
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/055,111
; FILING DATE: 06-AUG-1997
; APPLICATION NUMBER: US 09/062,866
; FILING DATE: 20-APR-1998
; APPLICATION NUMBER: US 09/097,976
; FILING DATE: 16-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0725K2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-852-9196
; TELEFAX: 650-496-1200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-770-528-10

Query Match          100.0%; Score 40; DB 9; Length 269;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAV 7
Db      113 YVHDAV 119

RESULT 50
US-10-139-833-7
; Sequence 7, Application US/10139833
; Publication No. US20030004106A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Christiaan M.
; APPLICANT: Giles, Jennifer
; APPLICANT: Mu, Sharon X.
; APPLICANT: Xia, Min
; APPLICANT: Bass, Michael B.
; APPLICANT: Craveiro, Roger
; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
; Uses Thereof
; FILE REFERENCE: 00-1213-E
; CURRENT APPLICATION NUMBER: US/10/139,833
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/170,191
; PRIOR FILING DATE: 1999-12-10
```

; PRIOR APPLICATION NUMBER: 60/188,053  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: 60/194,521  
; PRIOR FILING DATE: 2000-04-04  
; PRIOR APPLICATION NUMBER: 60/195,910  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: 09/724,583  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-139-833-7

Query Match 100.0%; Score 40; DB 14; Length 269;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 113 YVHDAPV 119  
|||||

RESULT 51  
US-10-011-931-2  
; Sequence 2, Application US/10011931  
; Publication No. US2003026806A1  
; GENERAL INFORMATION:  
; APPLICANT: WITTE, ALISON  
; APPLICANT: VARNUM, BRIAN C.  
; APPLICANT: QIAN, ZUENING  
; APPLICANT: VEZINA, CHRIS  
; TITLE OF INVENTION: ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING AGENTS THAT ALLOW BINDING OF IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF  
; TITLE OF INVENTION: IL-1 RECEPTOR BUT NOT ACTIVATION THEREOF  
; FILE REFERENCE: A-731  
; CURRENT APPLICATION NUMBER: US/10/011,931  
; CURRENT FILING DATE: 2002-04-01  
; PRIOR APPLICATION NUMBER: US 60/244,118  
; PRIOR FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-011-931-2

Query Match 100.0%; Score 40; DB 14; Length 269;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 113 YVHDAPV 119  
|||||

RESULT 52  
US-10-038-557A-2  
; Sequence 2, Application US/10038557A  
; Publication No. US2003002684A1  
; GENERAL INFORMATION:  
; APPLICANT: Fredeking, Terry M.  
; APPLICANT: Ignatyev, George M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS INFECTIONS AND OTHER DISORDERS  
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS  
; FILE REFERENCE: 24861-301D  
; CURRENT APPLICATION NUMBER: US/10/038,557A  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: 09/840,707  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: 09/562,979

; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/198,210  
; PRIOR FILING DATE: 1999-04-27  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Interleukin-1 beta (catabolin)  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: P01584/Genbank  
; DATABASE ENTRY DATE: 1986-07-21  
US-10-038-557A-2

Query Match 100.0%; Score 40; DB 14; Length 269;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 113 YVHDAPV 119  
|||||

RESULT 53  
US-10-167-127-4  
; Sequence 4, Application US/10167127  
; Publication No. US20030100031A1  
; GENERAL INFORMATION:  
; APPLICANT: DOWER, STEVEN  
; APPLICANT: DUFF, GORDON W.  
; TITLE OF INVENTION: INTEGRATIVE ASSAYS FOR MONITORING MOLECULAR ASSEMBLY  
; TITLE OF INVENTION: EVENTS  
; FILE REFERENCE: MSA-026.01 (20974-2601)  
; CURRENT APPLICATION NUMBER: US/10/167,127  
; CURRENT FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: 60/297,305  
; PRIOR FILING DATE: 2001-06-11  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-167-127-4

Query Match 100.0%; Score 40; DB 14; Length 269;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
Db 113 YVHDAPV 119  
|||||

RESULT 54  
US-10-440-464-53  
; Sequence 53, Application US/10440464  
; Publication No. US20040018528A1  
; GENERAL INFORMATION:  
; APPLICANT: DEPRIMO, SAMUEL  
; APPLICANT: O'FARRELL, ANNE-MARIE  
; APPLICANT: MORIMOTO, ALYSSA  
; APPLICANT: SMOLICH, BEVERLY  
; APPLICANT: MANNING, WILLIAM  
; APPLICANT: WALTER, SARAH  
; APPLICANT: CHERRINGTON, JULIE  
; APPLICANT: SCHILLING, JIM  
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE  
; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS  
; FILE REFERENCE: 038602/1592  
; CURRENT APPLICATION NUMBER: US/10/440,464



; CURRENT FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: 60/380,872  
; PRIOR FILING DATE: 2002-05-17  
; PRIOR APPLICATION NUMBER: 60/448,922  
; PRIOR FILING DATE: 2003-02-24  
; PRIOR APPLICATION NUMBER: 60/448,874  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 185  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-440-464-53

Query Match 100.0%; Score 40; DB 15; Length 269;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 113 YVHDAPV 119  
|||||

## RESULT 55

US-10-447-315-13  
; Sequence 13, Application US/10447315  
; Publication No. US20040071687A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafii, Shahin  
; APPLICANT: Heissig, Beate  
; APPLICANT: Hattori, Koichi  
; APPLICANT: Cornell Research Foundation, Inc.  
; TITLE OF INVENTION: Adult Stem Cell Recruitment  
; FILE REFERENCE: 1676.006US1  
; CURRENT APPLICATION NUMBER: US/10/447,315  
; CURRENT FILING DATE: 2003-05-28  
; PRIOR APPLICATION NUMBER: US 60/383,658  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-447-315-13

Query Match 100.0%; Score 40; DB 15; Length 269;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 113 YVHDAPV 119  
|||||

## RESULT 56

US-10-637-313-82  
; Sequence 82, Application US/10637313  
; Publication No. US20040229779A1  
; GENERAL INFORMATION:  
; APPLICANT: Ramesh Kekuda  
; APPLICANT: Uriel Malyankar  
; APPLICANT: Li Li  
; APPLICANT: David Anderson  
; APPLICANT: Sasha Guo  
; APPLICANT: Mei Zhong  
; APPLICANT: Muralidhara Padigaru  
; APPLICANT: Stacie Casman  
; APPLICANT: Ferenc Boldog  
; APPLICANT: Charles Miller  
; APPLICANT: Nikolai Khrantsov  
; APPLICANT: Corine Vernet

; APPLICANT: Meera Patturajan  
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
; FILE REFERENCE: 21402-593B  
; CURRENT APPLICATION NUMBER: US/10/637,313  
; CURRENT FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: 10/162335  
; PRIOR FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: 60/295607  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 60/295661  
; PRIOR FILING DATE: 2001-06-04  
; PRIOR APPLICATION NUMBER: 60/296404  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/296418  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/298285  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/298556  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/299949  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/300883  
; PRIOR FILING DATE: 2001-06-26  
; PRIOR APPLICATION NUMBER: 60/301550  
; PRIOR FILING DATE: 2001-06-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 255  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 82  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-637-313-82

Query Match 100.0%; Score 40; DB 16; Length 269;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
DB 113 YVHDAPV 119  
|||||

## RESULT 57

US-10-985-299-2  
; Sequence 2, Application US/10985299  
; Publication No. US20050084493A1  
; GENERAL INFORMATION:  
; APPLICANT: WITTE, ALISON  
; APPLICANT: VARNUM, BRIAN C.  
; APPLICANT: QIAN, ZUEMING  
; APPLICANT: VEZINA, CHRIS  
; TITLE OF INVENTION: SCREENING METHOD FOR ANTIBODIES AND OTHER SELECTIVE IL-1 BINDING  
; TITLE OF INVENTION: AGENTS THAT ALLOW BINDING TO IL-1 RECEPTOR BUT NOT ACTIVATION  
; FILE REFERENCE: A-731A  
; CURRENT APPLICATION NUMBER: US/10/985,299  
; CURRENT FILING DATE: 2004-11-09  
; PRIOR APPLICATION NUMBER: US 10/011,931  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 60/244,118  
; PRIOR FILING DATE: 2000-10-27  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 2  
; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-985-299-2

Query Match 100.0%; Score 40; DB 17; Length 269;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 YVHDAPV 7
DB     113 YVHDAPV 119

RESULT 58
US-10-491-997-84
; Sequence 84, Application US/10491997
; Publication No. US20050089957A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF INFLAMMATORY BOWEL DISORDERS
; FILE REFERENCE: P1915R1 US
; CURRENT APPLICATION NUMBER: US/10/491,997
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: PCT/US02/33070
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/340,083
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 84
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-491-997-84

Query Match      100.0%; Score 40; DB 17; Length 269;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
DB     113 YVHDAPV 119

RESULT 59
US-10-437-963-178722
; Sequence 178722, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 178722
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT4530_76250C.1.pap
US-10-437-963-178722

Query Match      92.5%; Score 37; DB 16; Length 67;
Best Local Similarity 85.7%; Pred. No. 6.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
DB     40 YVHDAPV 46

RESULT 60
US-09-747-287-207
; Sequence 207, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-9486000US
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 207
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide.
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid
US-09-747-287-207

Query Match      90.0%; Score 36; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YVHDAP 6
DB      6 YVHDAP 11

RESULT 61
US-09-780-575-4
; Sequence 4, Application US/09780575
; Publication No. US20010029024A1
; GENERAL INFORMATION:
; APPLICANT: KODADEK, THOMAS J.
; TITLE OF INVENTION: SELECTION OF PEPTIDES WITH ANTIBODY-LIKE PROPERTIES
; FILE REFERENCE: UTSD:566US
; CURRENT APPLICATION NUMBER: US/09/780,575
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/182,060
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-780-575-4

Query Match      90.0%; Score 36; DB 9; Length 20;
Best Local Similarity 85.7%; Pred. No. 3.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
DB      7 YVHDGPV 13
```

```

Query Match      85.0%; Score 34; DB 16; Length 156;
Best Local Similarity 71.4%; Pred. NO. 66;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YVHDAPV 7

```

```

Query Match      82.5%; Score 33; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 VHDAPV 7
        |||||
Db      5 VHDAPV 10

RESULT 65
US-09-747-287-99
; Sequence 99, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: KOMORIYA, AKIRA
; APPLICANT: PACKARD, BEVERLY S.
; TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
; FILE REFERENCE: 300-9486000S
; CURRENT APPLICATION NUMBER: US/09/747,287
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/349,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US08/802,981
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 18
; TYPE: PRT

```

; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide.  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4)..(4)  
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: Xaa is D form Tyr  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (14)..(14)  
; OTHER INFORMATION: Xaa is epsilon-aminocaproic acid  
US-09-747-287-99

Query Match 82.5%; Score 33; DB 10; Length 18;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
|:||||  
Db 7 VHDAPV 12

RESULT 66  
US-10-425-115-229242  
; Sequence 229242, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 229242  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_140660C.1.pap  
US-10-425-115-229242

Query Match 82.5%; Score 33; DB 16; Length 58;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:||||  
Db 45 YHQAPV 51

RESULT 67  
US-10-425-115-274088  
; Sequence 274088, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 274088  
; LENGTH: 78  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_181557C.1.pap  
US-10-425-115-274088

Query Match 82.5%; Score 33; DB 16; Length 78;  
Best Local Similarity 83.3%; Pred. No. 51;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:||||  
Db 37 YLHDAP 42

RESULT 68  
US-10-425-115-247918  
; Sequence 247918, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 247918  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_157689C.1.pap  
US-10-425-115-247918

Query Match 82.5%; Score 33; DB 16; Length 120;  
Best Local Similarity 83.3%; Pred. No. 79;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:||||  
Db 79 YLHDAP 84

RESULT 69  
US-10-320-797-3074  
; Sequence 3074, Application US/10320797  
; Publication No. US20040014955A1  
; GENERAL INFORMATION:  
; APPLICANT: Eroshkin, Alexey M.  
; APPLICANT: Zamudio, Carlos  
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND  
; FILE REFERENCE: 10182-021-999  
; CURRENT APPLICATION NUMBER: US/10/320,797  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: 60/341,261  
; PRIOR FILING DATE: 2001-12-17  
; NUMBER OF SEQ ID NOS: 3361  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3074  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Cryptococcus neoformans  
US-10-320-797-3074

Query Match 82.5%; Score 33; DB 15; Length 272;  
Best Local Similarity 71.4%; Pred. No. 1.9e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|:|  
Db 77 YLHDCPV 83

## RESULT 70

US-10-275-026A-56  
; Sequence 56, Application US/10275026A  
; Publication No. US20040087770A1

## ; GENERAL INFORMATION:

; APPLICANT: Tang, Christoph  
; TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use

; FILE REFERENCE: GJE-6436  
; CURRENT APPLICATION NUMBER: US/10/275,026A

; CURRENT FILING DATE: 2003-10-31

; PRIOR APPLICATION NUMBER: PCT/GB01/02003

; PRIOR FILING DATE: 2001-05-08

; PRIOR APPLICATION NUMBER: GB 0011108.8

; PRIOR FILING DATE: 2000-05-08

; NUMBER OF SEQ ID NOS: 214

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 56

; LENGTH: 419

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-10-275-026A-56

Query Match 82.5%; Score 33; DB 15; Length 419;

Best Local Similarity 71.4%; Pred. No. 2.9e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|:|  
Db 315 YVHDVPL 321

## RESULT 71

US-10-275-026A-110

; Sequence 110, Application US/10275026A

; Publication No. US20040087770A1

## ; GENERAL INFORMATION:

; APPLICANT: Tang, Christoph

; TITLE OF INVENTION: Virulence Genes, Proteins, and Their Use

; FILE REFERENCE: GJE-6436

; CURRENT APPLICATION NUMBER: US/10/275,026A

; CURRENT FILING DATE: 2003-10-31

; PRIOR APPLICATION NUMBER: PCT/GB01/02003

; PRIOR FILING DATE: 2001-05-08

; PRIOR APPLICATION NUMBER: GB 0011108.8

; PRIOR FILING DATE: 2000-05-08

; NUMBER OF SEQ ID NOS: 214

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 110

; LENGTH: 419

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-10-275-026A-110

Query Match 82.5%; Score 33; DB 15; Length 419;

Best Local Similarity 71.4%; Pred. No. 2.9e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|:|  
Db 315 YVHDVPL 321

## RESULT 72

US-10-437-963-152111

; Sequence 152111, Application US/10437963

; Publication No. US20040123343A1

## ; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

## ; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; SEQ ID NO 152111

; LENGTH: 45

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_52194C.1.pgp

US-10-437-963-152111

Query Match 80.0%; Score 32; DB 16; Length 45;

Best Local Similarity 83.3%; Pred. No. 45;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
|:|:|:|  
Db 31 IHDAPV 36

## RESULT 73

US-10-425-114-41734

; Sequence 41734, Application US/10425114

; Publication No. US20040034888A1

## ; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 41734

; LENGTH: 162

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLM017290D08\_FLI.pgp

US-10-425-114-41734

Query Match 80.0%; Score 32; DB 15; Length 162;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|:|  
Db 37 YVHEAP 42

## RESULT 74

US-10-732-923-21825

; Sequence 21825, Application US/10732923

; Publication No. US20050108791A1

## ; GENERAL INFORMATION:

; APPLICANT: Edgerton, Michael D

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 21825  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Lilium longiflorum  
US-10-732-923-21825

Query Match 80.0%; Score 32; DB 17; Length 203;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
Db 69 YAHAP 74

RESULT 75  
US-10-282-122A-71089  
; Sequence 71089, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Lianguo  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 71089  
; LENGTH: 213  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-10-282-122A-71089

Query Match 80.0%; Score 32; DB 15; Length 213;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YVHDAP 7  
| | | | |  
Db 161 YIHDFFI 167

RESULT 76  
US-10-424-599-248882  
; Sequence 248882, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 248882  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(344)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_66771C.1.pap  
US-10-424-599-248882

Query Match 80.0%; Score 32; DB 15; Length 344;  
Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
Db 257 YIHDSP 262

RESULT 77  
US-10-437-963-199932  
; Sequence 199932, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 199932  
; LENGTH: 676  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(676)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_95451C.1.pap  
US-10-437-963-199932

```
Query Match      80.0%; Score 32; DB 16; Length 676;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      497 YIHSAPI 503

RESULT 78
US-10-437-963-160601
; Sequence 160601, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 160601
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_59867C.1.pap
US-10-437-963-160601

Query Match      77.5%; Score 31; DB 16; Length 32;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAP 6
Db      12 YVHDRP 17

RESULT 79
US-10-179-784-20
; Sequence 20, Application US/10179784
; Publication No. US20030036647A1
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; APPLICANT: Sriskanda, Verl
; TITLE OF INVENTION: Pharmacological Targeting of Bacterial DNA Ligase
; TITLE OF INVENTION: For Treatment And Prevention of Bacterial Infections
; FILE REFERENCE: D6468
; CURRENT APPLICATION NUMBER: US/10/179,784
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/300,727
; PRIOR FILING DATE: 2001-06-24
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: domain Ia of NAD+-dependent DNA ligase
US-10-179-784-20

Query Match      77.5%; Score 31; DB 14; Length 60;
Best Local Similarity 71.4%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      17 YIHTAPI 23

RESULT 80
US-10-179-784-22
; Sequence 22, Application US/10179784
; Publication No. US20030036647A1
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; APPLICANT: Sriskanda, Verl
; TITLE OF INVENTION: Pharmacological Targeting of Bacterial DNA Ligase
; TITLE OF INVENTION: For Treatment And Prevention of Bacterial Infections
; FILE REFERENCE: D6468
; CURRENT APPLICATION NUMBER: US/10/179,784
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/300,727
; PRIOR FILING DATE: 2001-06-24
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 22
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: domain Ia of NAD+-dependent DNA ligase
US-10-179-784-22

Query Match      77.5%; Score 31; DB 14; Length 60;
Best Local Similarity 71.4%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      15 YVRDAPV 21

RESULT 81
US-10-424-599-218015
; Sequence 218015, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 218015
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_38895C.1.pap
US-10-424-599-218015

Query Match      77.5%; Score 31; DB 15; Length 66;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      17 YIHTAPI 23

RESULT 82
US-10-425-115-302375
```

```
Query Match      80.0%; Score 32; DB 16; Length 676;
Best Local Similarity 57.1%; Pred. No. 7.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 YVHDAPV 7
Db      497 YIHSAPI 503
```

```
RESULT 78
US-10-437-963-160601
; Sequence 160601, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 160601
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_59867C.1.pap
US-10-437-963-160601
```

```
Query Match      77.5%; Score 31; DB 16; Length 32;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 YVHDAP 6
Db      12 YVHDRP 17
```

```
RESULT 79
US-10-179-784-20
; Sequence 20, Application US/10179784
; Publication No. US20030036647A1
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; APPLICANT: Sriskanda, Verl
; TITLE OF INVENTION: Pharmacological Targeting of Bacterial DNA Ligase
; TITLE OF INVENTION: For Treatment And Prevention of Bacterial Infections
; FILE REFERENCE: D6468
; CURRENT APPLICATION NUMBER: US/10/179,784
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/300,727
; PRIOR FILING DATE: 2001-06-24
; NUMBER OF SEQ ID NOS: 41
; SEQ ID NO 20
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
; FEATURE:
; NAME/KEY: DOMAIN
; OTHER INFORMATION: domain Ia of NAD+-dependent DNA ligase
US-10-179-784-20
```

```
Query Match      77.5%; Score 31; DB 14; Length 60;
Best Local Similarity 71.4%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

; Sequence 102375, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 302375  
; LENGTH: 67  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_38841C.1.pep  
US-10-425-115-302375

Query Match 77.5%; Score 31; DB 16; Length 67;  
Best Local Similarity 71.4%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:| |||  
DB 20 YTHAAPV 26

RESULT 83  
US-10-425-115-330170  
; Sequence 330170, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 330170  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(92)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_64215C.1.pep  
US-10-425-115-330170

Query Match 77.5%; Score 31; DB 16; Length 92;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:| |||  
DB 72 YPHDAPM 78

RESULT 84  
US-10-424-599-191361  
; Sequence 191361, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 191361  
; LENGTH: 150  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(150)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_14819C.1.pep  
US-10-424-599-191361

Query Match 77.5%; Score 31; DB 15; Length 150;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:| |||  
DB 144 YIHEAP 149

RESULT 85  
US-10-425-115-189250  
; Sequence 189250, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 189250  
; LENGTH: 167  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_104182C.1.pep  
US-10-425-115-189250

Query Match 77.5%; Score 31; DB 16; Length 167;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:| |||  
DB 60 YVHDLP 65

RESULT 86  
US-10-425-115-272422  
; Sequence 272422, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B



; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 272422  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_180034C.1.pep  
US-10-425-115-272422

Query Match 77.5%; Score 31; DB 16; Length 223;  
Best Local Similarity 71.4%; Pred. No. 3.8e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|||||  
Db 94 YLYDAPV 100

RESULT 87  
US-10-425-114-47269  
; Sequence 47269, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 47269  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701172318\_FLI.pep  
US-10-425-114-47269

Query Match 77.5%; Score 31; DB 15; Length 232;  
Best Local Similarity 66.7%; Pred. No. 4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
|:|||||  
Db 28 IHDAPV 33

RESULT 88  
US-10-282-122A-53482  
; Sequence 53482, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53482  
; LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Clostridium difficile  
US-10-282-122A-53482

Query Match 77.5%; Score 31; DB 15; Length 259;  
Best Local Similarity 57.1%; Pred. No. 4.5e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|||||  
Db 76 YIHDPL 82

RESULT 89  
US-10-425-115-336817  
; Sequence 336817, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 336817  
; LENGTH: 267  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_70336C.1.pep  
US-10-425-115-336817

Query Match 77.5%; Score 31; DB 16; Length 267;  
Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|||||  
Db 64 HVHDAP 69

RESULT 90

US-10-425-115-350581  
; Sequence 350581, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 350581  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(288)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_82900C.1.pep  
US-10-425-115-350581

Query Match 77.5%; Score 31; DB 16; Length 288;  
Best Local Similarity 66.7%; Pred. No. 5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
:|||||  
DB 43 IHDAPV 48

RESULT 91  
US-10-424-599-195944  
; Sequence 195944, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 195944  
; LENGTH: 295  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(295)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_18964C.1.pep  
US-10-424-599-195944

Query Match 77.5%; Score 31; DB 15; Length 295;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|||||  
DB 108 YVHDLF 113

RESULT 92  
US-10-739-930-9926

; Sequence 9926, Application US/10739930  
; Publication No. US20040216190A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53377)B  
; CURRENT APPLICATION NUMBER: US/10/739,930  
; CURRENT FILING DATE: 2003-12-18  
; NUMBER OF SEQ ID NOS: 11088  
; SEQ ID NO 9926  
; LENGTH: 355  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; OTHER INFORMATION: Clone ID: TRIAB-23APR03-C21747\_1.p  
US-10-739-930-9926

Query Match 77.5%; Score 31; DB 16; Length 355;  
Best Local Similarity 71.4%; Pred. No. 6.2e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
:|||||  
DB 94 YLYDAPV 100

RESULT 93  
US-10-437-963-125228  
; Sequence 125228, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 125228  
; LENGTH: 363  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_27893C.1.p  
US-10-437-963-125228

Query Match 77.5%; Score 31; DB 16; Length 363;  
Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
:|||||  
DB 336 YIHDCP 341

RESULT 94  
US-10-437-963-144994  
; Sequence 144994, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei

```
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-04-28
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 144994
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45756C.1.pep
US-10-437-963-144994

Query Match          77.5%; Score 31; DB 16; Length 557;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAP 6
Db      235 YVHDLP 240

RESULT 95
US-10-425-115-197846
; Sequence 197846, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 197846
; LENGTH: 602
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(602)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112016C.1.pep
US-10-425-115-197846

Query Match          77.5%; Score 31; DB 16; Length 602;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAP 6
Db      148 YVHDLP 153

RESULT 96
US-10-425-114-59691
; Sequence 59691, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei

; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59691
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-211-F3_FLI.pep
US-10-425-114-59691

Query Match          77.5%; Score 31; DB 15; Length 619;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAP 6
Db      165 YVHDLP 170

RESULT 97
US-09-712-363-263
; Sequence 263, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-263

Query Match          77.5%; Score 31; DB 9; Length 691;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      32 YVRDAPV 38

RESULT 98
US-10-282-122A-62639
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; Sequence 62639, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62639
; LENGTH: 691
; TYPE: PRF
; ORGANISM: Mycobacterium bovis
US-10-282-122A-62639
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Query Match 77.5%; Score 31; DB 15; Length 691;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YVHDAPV 7
DB 32 YVRDAPV 38
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RESULT 99
US-10-282-122A-64828
; Sequence 64828, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
```

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; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64828
; LENGTH: 691
; TYPE: PRF
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64828
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Query Match 77.5%; Score 31; DB 15; Length 691;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 1 YVHDAPV 7
DB 32 YVRDAPV 38
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RESULT 100
US-10-282-122A-63922
; Sequence 63922, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
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; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63922
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-282-122A-63922

Query Match      77.5%; Score 31; DB 15; Length 694;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 YVHDAPV 7
Db      32 YVRDAPV 38
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Search completed: June 30, 2005, 22:35:50  
Job time : 165 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 22:13:54 ; Search time 39 Seconds  
(without alignments)  
17.270 Million cell updates/sec

Title: US-09-874-350C-210

Perfect score: 40

Sequence: 1 YVHDAPV 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

PIR 79:\*\*

1: piri:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	269	1 ICHU1B	interleukin-1 beta
2	35	87.5	321	2 D91037	glucokinase [impor
3	35	87.5	321	2 A65013	glucokinase [EC 2,
4	35	87.5	321	2 F85881	glucokinase [impor
5	33	82.5	361	2 C65132	hypothetical prote
6	33	82.5	419	1 S32880	lipB protein - Nei
7	33	82.5	419	2 G82012	capsule polysaccha
8	33	82.5	419	2 E81240	capsule polysaccha
9	33	82.5	730	2 T49736	hypothetical prote
10	33	82.5	735	2 T35810	probable DNA ligas
11	32	80.0	203	2 JC2207	hypothetical prote
12	32	80.0	206	2 T41232	hypothetical prote
13	32	80.0	228	2 B54676	antiquitin - rat (
14	32	80.0	295	2 C75054	methionyl aminopep
15	32	80.0	295	2 C71107	probable methionyl
16	32	80.0	306	2 AF1142	ABC transporter (b
17	32	80.0	306	2 A11500	ABC transporter (b
18	32	80.0	389	1 S36653	kpsD protein - Esc
19	32	80.0	454	2 AE1970	hypothetical prote
20	32	80.0	1871	2 D96698	probable DNA polym
21	32	80.0	1894	2 T02155	DNA-directed DNA p
22	32	80.0	3131	2 T39553	vacuolar protein s
23	31	77.5	169	2 B82757	transcription regu
24	31	77.5	242	2 C95296	hypothetical prote
25	31	77.5	321	2 T27521	hypothetical prote
26	31	77.5	388	2 B36792	hypothetical prote
27	31	77.5	496	2 C85789	hypothetical prote
28	31	77.5	496	2 F87423	ferredoxin, probab
29	31	77.5	556	2 B64939	hypothetical prote

30	31	77.5	556	2 G90940	hypothetical prote
31	31	77.5	560	2 H83206	probable decarboxy
32	31	77.5	634	2 AE2558	hypothetical prote
33	31	77.5	691	2 A70857	probable liga - My
34	31	77.5	694	2 T45403	DNA ligase [impor
35	31	77.5	1171	2 F83110	exodeoxyribonuclea
36	31	77.5	1293	1 A46350	RNA-directed RNA p
37	31	77.5	1294	2 S01085	hypothetical prote
38	30	75.0	83	2 D69153	hypothetical prote
39	30	75.0	101	2 AH0070	probable membrane
40	30	75.0	131	1 IMECN4	colicin N immunity
41	30	75.0	162	2 T38904	conserved hypotet
42	30	75.0	164	2 T11215	hypothetical prote
43	30	75.0	239	1 A41892	hydrogenase (EC 1.
44	30	75.0	244	1 C43255	hydrogenase (EC 1.
45	30	75.0	244	1 S39400	hydrogenase (EC 1.
46	30	75.0	251	2 F87242	probable secreted
47	30	75.0	251	2 D70840	hypothetical prote
48	30	75.0	271	2 D70915	hypothetical prote
49	30	75.0	311	2 D69881	yabc protein homol
50	30	75.0	336	2 E90063	conserved hypotet
51	30	75.0	367	2 AG0634	probable oxidoredu
52	30	75.0	374	2 E82168	probable alpha-1.6
53	30	75.0	453	2 B83242	hypothetical prote
54	30	75.0	474	2 S16727	coenzyme F420 hydr
55	30	75.0	480	2 AF2206	glutamyl-tRNA synt
56	30	75.0	515	2 G70941	hypothetical prote
57	30	75.0	548	2 AD1216	ABC transporters,
58	30	75.0	548	2 A11569	ABC transporters,
59	30	75.0	598	2 I51368	gamma-aminobutyric
60	30	75.0	628	2 T20714	hypothetical prote
61	30	75.0	677	2 AG2020	DNA ligase [impor
62	30	75.0	803	2 B56277	DNA-directed DNA p
63	30	75.0	833	2 S62136	CWH41 protein - ye
64	30	75.0	838	2 A38172	adenylate cyclase
65	30	75.0	843	2 AB0539	Rhs-family protein
66	30	75.0	874	2 T00491	capsid protein pre
67	30	75.0	965	2 AE0418	valine-tRNA ligase
68	30	75.0	1329	2 A64828	cell division prot
69	30	75.0	1342	2 E85614	cell division prot
70	30	75.0	1342	2 G90750	cell division prot
71	29	72.5	61	1 UPSCX	D-Xylose uptake pr
72	29	72.5	66	2 E69464	hypothetical prote
73	29	72.5	84	2 T09540	proline rich prote
74	29	72.5	117	2 G87460	hypothetical prote
75	29	72.5	161	2 F83297	hypothetical prote
76	29	72.5	180	2 S56944	probable membrane
77	29	72.5	180	2 A84347	hypothetical prote
78	29	72.5	182	2 F97499	hypothetical prote
79	29	72.5	196	2 H70726	probable holliday
80	29	72.5	210	2 T22344	hypothetical prote
81	29	72.5	214	2 A47581	septal cell wall d
82	29	72.5	217	2 T16559	hypothetical prote
83	29	72.5	218	2 T30415	host range factor
84	29	72.5	219	2 F83131	conserved hypotet
85	29	72.5	238	2 E70039	glycolate oxidase
86	29	72.5	242	2 AC0676	Ni/Fe-hydrogenase
87	29	72.5	252	2 JC5237	osmotin-like prote
88	29	72.5	261	1 PWYCA6	H+-transporting tw
89	29	72.5	264	2 AE3545	dipeptide transpor
90	29	72.5	271	2 S72782	Bi496 F2.81 protei
91	29	72.5	273	2 T17629	hypothetical prote
92	29	72.5	281	2 F83923	manganese-containi
93	29	72.5	289	1 PSECA1	phospholipase A1 (
94	29	72.5	289	2 A10917	detergent-resistan
95	29	72.5	289	2 E86069	outer membrane pho
96	29	72.5	289	2 G91222	outer membrane pho
97	29	72.5	289	2 A36971	phosphoribulokinase
98	29	72.5	291	1 K10XPR	formamidopyrimidin
99	29	72.5	291	2 H75512	hypothetical prote
100	29	72.5	303	2 S45461	hypothetical prote
101	29	72.5	324	2 E84972	hypothetical prote
102	29	72.5	326	2 T36497	probable branched-

103 29 72.5 340 2 T46112 hypothetical prote  
104 29 72.5 343 2 E88957 protein ZK697.11 [l  
105 29 72.5 349 2 I39535 Probable L-lactate  
106 29 72.5 356 2 F95357 Probable fatty aci  
107 29 72.5 359 2 A69057 conserved hypothet  
108 29 72.5 359 2 E87447 sulfate ABC transp  
109 29 72.5 366 2 S51363 actin modulator pr  
110 29 72.5 375 2 S3587 E2 protein - human  
111 29 72.5 376 2 A82676 conserved hypothet  
112 29 72.5 400 2 AC3401 cell wall degradat  
113 29 72.5 403 1 VCBBL coat protein precu  
114 29 72.5 405 2 AE0990 probable membrane  
115 29 72.5 414 2 T49916 hypothetical prote  
116 29 72.5 415 2 B70898 probable exonuclea  
117 29 72.5 419 2 B96833 hypothetical prote  
118 29 72.5 427 2 T06191 probable endo-1,4-  
119 29 72.5 443 2 AC3720 conserved hypothet  
120 29 72.5 443 2 G97501 probable amidase (  
121 29 72.5 446 2 AI0401 probable membrane  
122 29 72.5 468 2 C95405 Probable sulfite o  
123 29 72.5 471 2 F72257 lipopolysaccharide  
124 29 72.5 482 2 F96778 hypothetical prote  
125 29 72.5 488 2 E82161 succinate-semialde  
126 29 72.5 489 2 G64039 hypothetical prote  
127 29 72.5 494 2 T16658 hypothetical prote  
128 29 72.5 502 2 F87436 peptidoglycan bind  
129 29 72.5 514 1 A47692 fumarate hydratase  
130 29 72.5 515 2 E72474 hypothetical prote  
131 29 72.5 516 2 S52815 probable membrane  
132 29 72.5 522 2 B75289 hypothetical prote  
133 29 72.5 524 2 D82220 conserved hypothet  
134 29 72.5 531 2 AH3378 cell wall degradat  
135 29 72.5 539 1 S48474 glucan 1,4-alpha-g  
136 29 72.5 549 1 S19095 transcription fact  
137 29 72.5 553 2 T52362 hypothetical prote  
138 29 72.5 570 2 AC2356 hypothetical prote  
139 29 72.5 582 2 T46822 phytoene desaturase  
140 29 72.5 590 2 A26638 homeotic protein D  
141 29 72.5 613 2 JS0763 triacylglycerol li  
142 29 72.5 615 2 AI0615 probable exported  
143 29 72.5 615 2 H90754 probable amidase (  
144 29 72.5 615 2 F85618 probable amidase y  
145 29 72.5 615 2 D64832 ycbB protein precu  
146 29 72.5 618 2 AI0171 probable exported  
147 29 72.5 621 2 H87662 feruloyl-CoA synth  
148 29 72.5 622 2 T23541 hypothetical prote  
149 29 72.5 642 2 A97555 probable amidase (  
150 29 72.5 642 2 AC2775 conserved hypothet

## ALIGNMENTS

RESULT 1  
ICHU1B  
interleukin-1 beta precursor [validated] - human  
N;Alternate names: hematoopoietin-1; IL-1 beta  
C;Species: Homo sapiens (man)  
C;Date: 28-Feb-1986 #sequence revision 15-May-1998 #text change 09-Jul-2004  
C;Accession: A25542; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S19  
R;Clark, B. D.; Collins, K. L.; Gandy, M. S.; Webb, A. C.; Auron, P. E.  
Nucleic Acids Res. 14, 7897-7914, 1986  
A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a rev  
A;Reference number: A25542; PMID:87040762; PMID:3490654  
A;Accession: A25542  
A;Molecule type: DNA; mRNA  
A;Residues: 1-5,'K',7-269 <CLA>  
A;Cross-references: UNIPROT:P01584; GB:X04500; NID:g33788  
A;Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu  
R;Bensi, G.; Raugeli, G.; Falla, E.; Carinci, V.; Buonamassa, D. T.; Meili, M.  
Gene 52, 95-101, 1987  
A;Title: Human interleukin-1 beta gene.  
A;Reference number: A29019; PMID:87248099; PMID:2954882

A;Accession: A29019  
A;Molecule type: DNA  
A;Residues: 1-269 <BEN>  
A;Cross-references: GB:M15840; NID:g186281; PIDN:AAA74137.1; PID:g386816  
R;Auron, P. E.; Webb, A. C.; Rosenwasser, L. J.; Mucci, S. F.; Rich, A.; Wolff, S. M.; Dinare  
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984  
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
A;Reference number: A94023; PMID:85089517; PMID:6083565  
A;Accession: A94023  
A;Molecule type: mRNA  
A;Residues: 1-5,'K',7-269 <AUR>  
A;Cross-references: GB:K02770; NID:g186268; PIDN:AAA36106.1; PID:g307043  
R;March, C. J.; Mosley, B.; Larsen, A.; Cerretti, D. P.; Braedt, G.; Price, V.; Gillis, S.  
Nature 315, 641-647, 1985  
A;Title: Cloning, sequence and expression of two distinct human interleukin-1 complement  
A;Reference number: A93361; PMID:85240547; PMID:2989698  
A;Accession: A93361  
A;Molecule type: mRNA  
A;Residues: 1-269 <MAR>  
A;Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790  
A;Note: parts of this sequence, including the amino end of the mature form, were confirm  
R;Webb, A. C.; Dinarello, C. A.; Rosenwasser, L. J.; Mucci, S. F.; Rich, A.; Wolff, S. M.; A  
Adv. Gene Technol. 22, 339-340, 1985  
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.  
A;Reference number: I51852  
A;Accession: I51852  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-5,'K',7-19,'H',21-110,'Q',112-176,'A',178-213,'P',215-269 <WEB>  
A;Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288  
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hira  
Biochem. Biophys. Res. Commun. 143, 345-352, 1987  
A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.  
A;Reference number: I52217; PMID:87156769; PMID:3493774  
A;Accession: I52217  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-269 <NIS>  
A;Cross-references: GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045  
R;Kotenko, S. V.; Bulemkov, M. T.; Veiko, V. P.; Epishin, S. M.; Lomakin, I. B.; Emel'yanov,  
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989  
A;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin  
A;Reference number: I38131; PMID:90249285; PMID:2635664  
A;Accession: I38132  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-269 <KOT>  
A;Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663  
R;Zsebo, K. M.; Wypych, J.; Yuschekoff, V. N.; Lu, H.; Hunt, P.; Dukes, P. P.; Langley, K.  
Blood 71, 962-968, 1988  
A;Title: Effects of hematoopoietin-1 and interleukin 1 activities on early hematopoietic  
A;Reference number: A90732; PMID:88184226; PMID:3281727  
A;Accession: B27616  
A;Molecule type: protein  
A;Residues: 117-123,'X',125-126,'X',128 <ZSE>  
R;Stevenson, F. T.; Bursten, S. L.; Pantou, C.; Locksley, R. M.; Lovett, D. H.  
Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993  
A;Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysine  
A;Reference number: A48293; PMID:93348250; PMID:8346241  
A;Contents: annotation; myristylation of lysines  
R;Nanduri, V. B.; Hulmes, J. D.; Pan, Y. C. E.; Kilian, P. L.; Stern, A. S.  
Biochim. Biophys. Acta 1118, 25-35, 1991  
A;Title: The role of arginine residues in interleukin 1 receptor binding.  
A;Reference number: S19608; PMID:92110334; PMID:1837236  
A;Contents: annotation; type 1 IL-1 receptor interaction site  
A;Note: modification of Arg-120 by phenylglyoxal blocks receptor binding  
R;Clare, G. M.; Gronenborn, A. M.  
submitted to the Brookhaven Protein Data Bank, January 1991  
A;Reference number: A50049; PDB:1B1B  
A;Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269  
R;Clare, G. M.; Wingfield, P. T.; Gronenborn, A. M.  
Biochemistry 30, 2315-2323, 1991



A;Title: High-resolution three-dimensional structure of interleukin beta in solution by  
A;Reference number: A44675; MUID:91159409; PMID:2001363  
A;Contents: annotation; (1)H-NMR structural determination  
R;Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R.  
J. Biol. Chem. 266, 7081-7086, 1991  
A;Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a con  
A;Reference number: A39774; MUID:91201363; PMID:2016316  
A;Contents: annotation  
R;Finzel, B.C.; Watenpugh, K.D.; Einspahr, H.M.  
submitted to the Broomhaven Protein Data Bank, December 1989  
A;Reference number: A50016; PDB:111B  
R;Finzel, B.C.; Clancy, L.B.; Holland, D.R.; Muchmore, S.W.; Watenpugh, K.D.; Einspahr,  
J. Mol. Biol. 209, 779-791, 1989  
A;Title: Crystal structure of recombinant human interleukin-lbeta at 2.0 angstrom resolu  
A;Reference number: A44666; MUID:90064532; PMID:2585509  
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269  
R;Finzel, B.C.; Clancy, L.B.; Holland, D.R.; Muchmore, S.W.; Watenpugh, K.D.; Einspahr,  
J. Mol. Biol. 209, 779-791, 1989  
A;Title: Crystal structure of recombinant human interleukin-lbeta at 2.0 angstrom resolu  
A;Reference number: A44666; MUID:90064532; PMID:2585509  
A;Contents: annotation; X-ray crystallography, 2.0 angstroms  
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag  
ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.  
C;Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-la  
C;Genetics:  
A;Gene: GDB:IL1B  
A;Cross-references: GDB:120094; OMIM:147720  
A;Map position: 2q13-2q21  
A;Introns: 16/2; 33/3; 101/1; 156/1; 199/3  
C;Superfamily: Interleukin-1  
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag  
F;117-269/Product: interleukin-1 beta #status experimental <ILI>  
F;76/Binding site: myristate (lys) (partial) #status experimental  
F;123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 100.0%; Score 40; DB 1; Length 269;  
Best Local Similarity 100.0%; Pred. No. 0.92;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||||  
DB 113 YVHDAPV 119

RESULT 2  
D91037  
glucokinase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: D91037  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: D91037  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-321 <HAY>  
A;Cross-references: UNIPROT:P46880; GB:BA000007; PIDN:BA036691.1; PID:G13362738; GSPDB:G  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: ECs3268  
C;Superfamily: glucokinase

Query Match 87.5%; Score 35; DB 2; Length 321;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||||  
DB 290 YVHDIPV 296

RESULT 3  
A65013  
glucokinase (EC 2.7.1.2) - Escherichia coli (strain K-12)

C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: A65013  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: A65013  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-321 <BLAT>  
A;Cross-references: UNIPROT:P46880; GB:AE000327; GB:U00096; NID:G1788731; PIDN:AAC75447  
A;Experimental source: strain K-12, substrain MG1655  
C;Genetics:  
A;Gene: glk  
C;Superfamily: glucokinase  
C;Keywords: phosphotransferase

Query Match 87.5%; Score 35; DB 2; Length 321;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||||  
DB 290 YVHDIPV 296

RESULT 4  
F85881  
glucokinase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: F85881  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: F85881  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-321 <STO>  
A;Cross-references: UNIPROT:P46880; GB:AE005174; NID:G12516765; PIDN:AAG57514.1; GSPDB:G  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: glk  
C;Superfamily: glucokinase

Query Match 87.5%; Score 35; DB 2; Length 321;  
Best Local Similarity 85.7%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||||  
DB 290 YVHDIPV 296

RESULT 5  
C65132  
hypothetical 38.6 kD protein in cysG-trpS intergenic region - Escherichia coli (strain  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: C65132  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C  
.A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: C65132  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-361 <BLAT>

A:Cross-references: UNIPROT:P45545; GB:AE000413; GB:U00096; NID:G2367215; PIDN:AACT6401.  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: ynfS

Query Match 82.5%; Score 33; DB 2; Length 361;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
 Db 95 VHDAPV 100  
 |||||  
 |||||

RESULT 6  
 S32880  
 lipB protein - Neisseria meningitidis  
 C:Species: Neisseria meningitidis  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: S32880; S28078  
 R:Frosch, M.; Mueller, A.  
 Mol. Microbiol. 8, 483-493, 1993  
 A:Title: Phospholipid substitution of capsular polysaccharides and mechanisms of capsule  
 A:Reference number: S32879; MUID:93316845; PMID:8326861  
 A:Accession: S32880  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-419 <PRO>  
 A:Cross-references: UNIPROT:Q93JTO; EMBL:Z13995  
 C:Genetics:  
 A:Gene: lipB  
 C:Superfamily: kpsD protein

Query Match 82.5%; Score 33; DB 1; Length 419;  
 Best Local Similarity 71.4%; Pred. No. 43;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 315 YVHDVPL 321  
 |||||  
 |||||

RESULT 7  
 G82012  
 capsule polysaccharide modification protein NWA0185 [imported] - Neisseria meningitidis  
 C:Species: Neisseria meningitidis  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
 C:Accession: G82012  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A:Reference number: A81775; MUID:20222556; PMID:10761919  
 A:Accession: G82012  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-419 <PAR>  
 A:Cross-references: UNIPROT:P57038; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB8350  
 A:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 A:Gene: lipB; NWA0185  
 C:Superfamily: kpsD protein

Query Match 82.5%; Score 33; DB 2; Length 419;  
 Best Local Similarity 71.4%; Pred. No. 43;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 315 YVHDVPL 321  
 |||||  
 |||||

RESULT 8

E81240  
 capsule polysaccharide modification protein LipB NMB0083 [imported] - Neisseria meningitidis  
 C:Species: Neisseria meningitidis  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
 C:Accession: E81240  
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
 A:Reference number: A81000; MUID:20175755; PMID:10710307  
 A:Accession: E81240  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-419 <TET>  
 A:Cross-references: UNIPROT:Q05014; GB:AE002368; GB:AE002098; NID:G7225303; PIDN:AAF4054  
 A:Experimental source: serogroup B, strain MC58  
 C:Genetics:  
 A:Gene: NMB0083  
 C:Superfamily: kpsD protein

Query Match 82.5%; Score 33; DB 2; Length 419;  
 Best Local Similarity 71.4%; Pred. No. 43;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 Db 315 YVHDVPL 321  
 |||||  
 |||||

RESULT 9  
 T49736  
 hypothetical protein B24B19.80 [imported] - Neurospora crassa  
 C:Species: Neurospora crassa  
 C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 15-Mar-2004  
 C:Accession: T49736  
 R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,  
 submitted to the Protein Sequence Database, May 2000  
 A:Reference number: Z25022  
 A:Accession: T49736  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-730 <SCH>  
 A:Cross-references: EMBL:AL356192; GSPDB:GN00116; NCSP:B24B19.80  
 A:Experimental source: BAC clone B24B19; strain OR74A  
 C:Genetics:  
 A:Gene: NCSP:B24B19.80  
 A:Map position: 6  
 A:Introns: 86/1  
 F:70-108/Domain: GML4 zinc binuclear cluster homology <GLA>

Query Match 82.5%; Score 33; DB 2; Length 730;  
 Best Local Similarity 83.3%; Pred. No. 79;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
 Db 113 YLHDAP 118  
 |||||  
 |||||

RESULT 10  
 T35810  
 probable DNA ligase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 12-Jul-2004  
 C:Accession: T35810  
 R:Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, February 1999  
 A:Reference number: Z21589  
 A:Accession: T35810  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

A;Residues: 1-735 <MUR>  
A;Cross-references: UNIPROT:Q9Z585; EMBL:AL035569; PIDN:CAB37570.1; GSPDB:GNO00070; SCOPED  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: ligA; SCOPEDB:SCBD9.06  
C;Superfamily: NAD+-dependent DNA ligase, ligA type

Query Match 82.5%; Score 33; DB 2; Length 735;  
Best Local Similarity 85.7%; Pred. No. 80;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
||:||||  
Db 39 YVNDAPV 45

RESULT 11  
JC2207  
Lim11 protein - trumpet lily  
C;Species: Lilium longiflorum (trumpet lily)  
C;Date: 19-Jul-1994 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: JC2207  
R;Kobayashi, T.; Kobayashi, E.; Sato, S.; Hotta, Y.; Miyajima, N.; Tanaka, A.; Tabata, S.  
DNA Res. 1, 15-26, 1994  
A;Title: Characterization of cDNAs induced in meiotic prophase in lily microsporocytes.  
A;Reference number: JC2207  
A;Accession: JC2207  
A;Molecule type: mRNA  
A;Residues: 1-203 <KOB>  
A;Cross-references: UNIPROT:Q43544; DBJ:D21817; NID:g431171; PIDN:BAA04841.1; PID:g4311  
A;Experimental source: Floral bud, meiotic prophase  
A;Note: The authors translated the codon CAG for residue 40 as His  
C;Genetics:  
A;Gene: LIM11

Query Match 80.0%; Score 32; DB 2; Length 203;  
Best Local Similarity 83.3%; Pred. No. 31;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
||:||||  
Db 69 YAHAP 74

RESULT 12  
T41232  
hypothetical protein SPCC1919.07 - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T41232  
R;Lyne, M.; Harris, D.E.; Murphey, L.D.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, January 1999  
A;Reference number: Z21979  
A;Accession: T41232  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-206 <LYN>  
A;Cross-references: UNIPROT:O94475; EMBL:AL035075; PIDN:CAA22638.1; GSPDB:GNO00068; SPDB:  
A;Experimental source: strain 972h-; cosmid c1919  
C;Genetics:  
A;Gene: SPDB:SPCC1919.07  
A;Map position: 3

Query Match 80.0%; Score 32; DB 2; Length 206;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
||:||||  
Db 21 IHDAPV 26

RESULT 13

B54676  
antiqutin - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: B54676  
R;Lee, P.; Kuhl, W.; Gelbart, T.; Kamimura, T.; West, C.; Beutler, E.  
Genomics 21, 371-378, 1994  
A;Title: Homology between a human protein and a protein of the green garden pea.  
A;Reference number: A54676; MUID:94375061; PMID:8088832  
A;Accession: B54676  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-228 <LEE>  
A;Cross-references: UNIPROT:Q64057; GB:S75019  
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 80.0%; Score 32; DB 2; Length 228;  
Best Local Similarity 83.3%; Pred. No. 36;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
||:||||  
Db 107 VHDAPV 112

RESULT 14  
C75054  
methionyl aminopeptidase (EC 3.4.11.18) map PAB1434 - Pyrococcus abyssi (strain Orsay)  
C;Species: Pyrococcus abyssi  
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C;Accession: C75054  
R;anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str  
A;Reference number: A75001  
A;Accession: C75054  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-295 <KAW>  
A;Cross-references: UNIPROT:Q9UYT4; GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB503  
A;Experimental source: strain Orsay  
C;Genetics:  
A;Gene: PAB1434  
C;Superfamily: Escherichia coli methionyl aminopeptidase  
C;Keywords: aminopeptidase

Query Match 80.0%; Score 32; DB 2; Length 295;  
Best Local Similarity 85.7%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
||:||||  
Db 208 YVRDAPV 214

RESULT 15  
C71107  
probable methionyl aminopeptidase - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
C;Accession: C71107  
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki,  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: C71107  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-295 <KAW>  
A;Cross-references: UNIPROT:O58362; GB:AP000003; NID:g3236130; PIDN:BAA29717.1; PID:g32  
A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

```
C:Genetics:
A:Gene: PH0628

Query Match      80.0%; Score 32; DB 2; Length 295;
Best Local Similarity 85.7%; Pred. No. 47;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 208 YVRDAPV 214

RESULT 16
AF1142
ABC transporter (binding protein) homolog lmo0541 [imported] - Listeria monocytogenes (s
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1142
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1142
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <GLA>
A:Cross-references: UNIPROT:Q8Y917; GB:NC_003210; PIDN:CAC98620.1; PID:gl6409917; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0541
C:Superfamily: Bacillus subtilis ferrichrome ABC transporter fhud

Query Match      80.0%; Score 32; DB 2; Length 306;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 198 YVHDAKV 204

RESULT 17
AI1500
ABC transporter (binding protein) homolog lin0545 [imported] - Listeria innocua (strain
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AI1500
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AI1500
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-306 <GLA>
A:Cross-references: UNIPROT:Q92EB5; GB:AL592022; PIDN:CAC95777.1; PID:gl6412985; GSPDB:G
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: lin0545

Query Match      80.0%; Score 32; DB 2; Length 306;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
```

---

```
Db 198 YVHDAKV 204

RESULT 18
S36653
kpsD protein - Escherichia coli
C:Species: Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S36653; E48492; C42644
R:Roberts, I.S.
submitted to the EMBL Data Library, August 1993
A:Reference number: S36649
A:Accession: S36653
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-389 <ROB>
A:Cross-references: UNIPROT:P42218; EMBL:X74567; NID:g997404; PIDN:CAAS2659.1; PID:g93974
R:Pazzani, C.; Rosenow, C.; Boulinois, G.J.; Bronner, D.; Jann, K.; Roberts, I.S.
J. Bacteriol. 175, 5978-5983, 1993
A:Title: Molecular analysis of region 1 of the Escherichia coli K5 antigen gene cluster
A:Reference number: A48492; MUID:93388530; PMID:8397187
A:Accession: E48492
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 22-389 <PAZ>
A:Cross-references: GB:X74567
R:Steenbergen, S.M.; Wrona, T.J.; Vimr, E.R.
J. Bacteriol. 174, 1099-1108, 1992
A:Title: Functional analysis of the stalyltransferase complexes in Escherichia coli K1 a
A:Reference number: A42644; MUID:92138601; PMID:1735705
A:Accession: C42644
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 106-125, 'D', 127-244, 'N', 246-297, 'S', 299-300, 'VI', 303-379, 'M', 381-385, 'W', 387
A:Cross-references: GB:M76370; NID:g146947; PIDN:AAA24214.1; PID:g146950
A:Experimental source: KL, strain EV1
A:Note: sequence extracted from NCBI backbone (NCBIN:79370, NCBIIP:79381)
C:Genetics:
A:Gene: kpsD
C:Superfamily: kpsD protein

Query Match      80.0%; Score 32; DB 1; Length 389;
Best Local Similarity 71.4%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 303 YVHDLPM 309

RESULT 19
AE1970
hypothetical protein alr1312 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AE1970
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, I.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1970
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <KUR>
A:Cross-references: UNIPROT:Q8YXA3; GB:BA000019; PIDN:BAW73269.1; PID:gl7130659; GSPDB:
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1312
C:Superfamily: conserved hypothetical protein b0835
```

Query Match 80.0%; Score 32; DB 2; Length 454;  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
 |||||  
 Db 229 YVHDVP 234

RESULT 20  
 D96698  
 probable DNA polymerase zeta catalytic subunit F12B7.5 [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C;Accession: D96698  
 R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; angen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: D96698  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-1871 <STO>  
 A;Cross-references: UNIPROT:Q9CAG6; GB:AE005173; NID:g6382521; PIDN:AAF07803.1; GSPDB:GN  
 C;Genetics:  
 A;Gene: F12B7.5  
 A;Map position: 1

Query Match 80.0%; Score 32; DB 2; Length 1871;  
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
 |||||  
 Db 329 VHDAP1 334

RESULT 21  
 T02155  
 DNA-directed DNA polymerase homolog TLF15.3 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
 C;Accession: T02155  
 R;Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Oji, O.; Kwan, A.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N submitted to the EMBL Data Library, June 1998  
 A;Description: Arabidopsis thaliana chromosome 1 BAC TLF15 sequence.  
 A;Reference number: Z14591  
 A;Accession: T02155  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1894 <VVS>  
 A;Cross-references: UNIPROT:O64795; EMBL:AC004393; NID:g3108024; PID:g3176661; GSPDB:GNC  
 A;Experimental source: cultivar Columbia  
 C;Genetics:  
 A;Gene: ATSP:TLF15.3  
 A;Map position: 1  
 A;Introns: 38/1; 65/3; 85/1; 101/3; 141/3; 158/3; 181/3; 229/3; 291/1; 321/3; 862/1; 926

Query Match 80.0%; Score 32; DB 2; Length 1894;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
 |||||  
 Db 329 VHDAP1 334

## RESULT 22

T39553  
 vacuolar protein sorting-associated protein - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C;Accession: T39553  
 R;Furnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998  
 A;Reference number: Z21863  
 A;Accession: T39553  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-3131 <PUR>  
 A;Cross-references: UNIPROT:O42926; EMBL:AL021767; PIDN:CAA16910.1; GSPDB:GN00067; SPDB  
 A;Experimental source: strain 972h-; cosmid c16C6  
 C;Genetics:  
 A;Gene: SPDB:SPBC16C6.02C  
 A;Map position: 2  
 A;Introns: 8/1; 45/3; 96/3; 2958/3

Query Match 80.0%; Score 32; DB 2; Length 3131;  
 Best Local Similarity 83.3%; Pred. No. 6.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7

Db 2650 IHDAPV 2655  
 :|||||

## RESULT 23

B82757  
 transcription regulator Fur family XF0821 [imported] - Xylella fastidiosa (strain 955c)  
 C;Species: Xylella fastidiosa  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C;Accession: B82757  
 R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequ Nature 406, 151-157, 2000  
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A;Reference number: A82515; MUID:20365717; PMID:10910347  
 A;Note: for a complete list of authors see reference number A59328 below  
 A;Accession: B82757  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-169 <SIM>  
 A;Cross-references: UNIPROT:Q9PE57; GB:AE003849; NID:g9105722; PIDN:AAF836  
 A;Experimental source: strain 955c  
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000  
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh J.D.; Junqueira, M.B.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.D.; Marques, M.V.; Martins, A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y. , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328  
 A;Experimental source: annotation  
 C;Genetics:  
 A;Gene: XF0821

Query Match 77.5%; Score 31; DB 2; Length 169;  
 Best Local Similarity 83.3%; Pred. No. 41;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6

Db 13 HVHDAP 18  
 :|||||

RESULT 24  
C95296  
hypothetical protein Sma0522 [imported] - Sinorhizobium meliloti (strain 1021) magaplasma  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: C95296  
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe  
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: C95296  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-242 <KUR>  
A:Cross-references: UNIPROT:Q930C3; GB:AE006469; PIDN:AAK64933.1; PID:gi4523355; GSPDB:G  
A:Experimental source: strain 1021, megaplasmid pSymA  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Sma0522  
A:Genome: plasmid

Query Match 77.5%; Score 31; DB 2; Length 242;  
Best Local Similarity 85.7%; Pred. No. 61;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YVHDAPV 7  
|||  
95 YVSDAPV 101  
  
RESULT 25  
T27521  
hypothetical protein ZC373.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T27521  
R:Kershaw, J.  
submitted to the EMBL Data Library, April 1995  
A:Reference number: Z20382  
A:Accession: T27521  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-321 <WIL>  
A:Cross-references: UNIPROT:Q23259; EMBL:Z49131; PIDN:CAA88975.1; GSPDB:GN00028; CBSP:ZC  
A:Experimental source: clone ZC373  
C:Genetics:  
A:Gene: CBSP:ZC373.3  
A:Map position: X  
A:Introns: 114/1, 174/3; 257/3

Query Match 77.5%; Score 31; DB 2; Length 321;  
Best Local Similarity 83.3%; Pred. No. 84;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YVHDAP 6  
|||  
91 YCHDAP 96  
  
RESULT 26  
B36792  
hypothetical protein 55 - ictaluriid herpesvirus 1 (strain auburn 1)  
C:Species: ictaluriid herpesvirus 1

A:Note: host Ictalurus punctatus (Channel catfish)  
C:Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: B36792  
R:Davidson, A.J.

submitted to GenBank, January 1992  
A:Description: Channel catfish virus: a new type of herpesvirus.  
A:Reference number: A36804  
A:Accession: B36792  
A:Molecule type: DNA  
A:Residues: 1-388 <DAV>  
A:Cross-references: UNIPROT:Q00153; GB:M75136; NID:g331209; PIDN:AAA88158.1; PID:g331265  
R:Davidson, A.J.  
Virology 186, 9-14, 1992  
A:Title: Channel catfish virus: a new type of herpesvirus.  
A:Reference number: A39447; MUID:92087490; PMID:1727613  
A:Contents: annotation  
A:Note: neither protein nor nucleic acid sequence is given  
C:Genetics:  
A:Gene: 55  
C:Superfamily: ictaluriid herpesvirus 1 hypothetical protein 55

Query Match 77.5%; Score 31; DB 2; Length 388;  
Best Local Similarity 85.7%; Pred. No. 1e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YVHDAPV 7  
|||  
364 YVKDAPV 370  
  
Db

RESULT 27  
C85789  
hypothetical protein 'yeaJ' [imported] - Escherichia coli (strain O157:H7, substrain EDL5  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: C85789  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: C85789  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-496 <STO>  
A:Cross-references: UNIPROT:Q8XDT6; GB:AE005174; NID:gi2515823; PIDN:AAG56775.1; GSPDB:G  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: 'yeaJ'  
C:Superfamily: hypothetical protein b1786

Query Match 77.5%; Score 31; DB 2; Length 496;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YVHDAP 6  
|||  
289 YVHDLP 294  
  
Db

RESULT 28  
F87423  
ferredoxin, probable [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: F87423  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: F87423

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-496 <STO>  
A;Cross-references: UNIPROT:Q9A8E9; GB:AB005673; NID:g13422764; PIDN:AAK23386.1; GSPDB:G  
C;Genetics:  
A;Gene: CC1405  
C;Superfamily: nitrogen fixation protein fixG; ferredoxin 2[4Fe-4S] homology

Query Match 77.5%; Score 31; DB 2; Length 496;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
DB 194 YFHDAP 199

RESULT 29  
B64939  
hypothetical protein b1786 - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
C;Accession: B64939  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: B64939  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-556 <BLAT>  
A;Cross-references: GB:AB000273; GB:U00096; NID:g1788078; PIDN:AACT4856.1; PID:g1788086;  
A;Experimental source: strain K-12, substrain MG1655  
C;Superfamily: hypothetical protein b1786

Query Match 77.5%; Score 31; DB 2; Length 556;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
DB 349 YVHDLDP 354

RESULT 30  
G90940  
hypothetical protein ECs2495 [imported] - Escherichia coli (strain O157:H7, substrain R  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: G90940  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawara, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: G90940  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-556 <HAY>  
A;Cross-references: UNIPROT:Q8XDT6; GB:BA000007; PIDN:BA035918.1; PID:g13361962; GSPDB:G  
A;Experimental source: strain O157:H7, substrain RMD 0509952  
C;Genetics:  
A;Gene: ECs2495  
C;Superfamily: hypothetical protein b1786

Query Match 77.5%; Score 31; DB 2; Length 556;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
DB 349 YVHDLDP 354

RESULT 31  
H83206  
probable decarboxylase PA3506 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 12-Jul-2004  
C;Accession: H83206  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: H83206  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-560 <STO>  
A;Cross-references: UNIPROT:Q9HYA3; GB:AE004771; GB:AE004091; NID:g9949650; PIDN:AA0606  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA3506  
C;Superfamily: acetolactate synthase, large subunit/pyruvate oxidase

Query Match 77.5%; Score 31; DB 2; Length 560;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
DB 117 YIHEAP 122

RESULT 32  
AE2558  
hypothetical protein alr8060 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC71209  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AE2558  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriq  
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AE2558  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-634 <KUR>  
A;Cross-references: UNIPROT:Q8YK57; GB:AP003603; PIDN:BA077390.1; PID:g17134833; GSPDB:G  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr8060  
A;Genome: plasmid

Query Match 77.5%; Score 31; DB 2; Length 634;  
Best Local Similarity 66.7%; Pred. No. 1.8e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
| | | | |  
DB 59 IHDAPV 64

RESULT 33  
A70857  
probable ligA - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 12-Jul-2004  
C;Accession: A70857  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998  
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: A70857  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-691 <COL>  
A:Cross-references: UNIPROT:053261; GB:AL021287; GB:AL123456; NID:g3261508; PIDN:CAA1609  
A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: ligA  
C:Superfamily: NAD+-dependent DNA ligase, Liga type

Query Match 77.5%; Score 31; DB 2; Length 691;  
Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
|||  
32 YVRDAPV 38

Db

RESULT 34  
T45403  
DNA ligase [imported] - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C:Date: 31-Jan-2000 #sequence\_revision 31-Jan-2000 #text\_change 12-Jul-2004  
A:Accession: T45403  
R:Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z16918  
A:Accession: T45403  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-694 <PAR>  
A:Cross-references: UNIPROT:033102; EMBL:Z99263; PIDN:CAB16425.1  
A:Experimental source: cosmid B637  
C:Genetics:  
A:Note: lig  
C:Superfamily: NAD+-dependent DNA ligase, Liga type

Query Match 77.5%; Score 31; DB 2; Length 694;  
Best Local Similarity 71.4%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
|||  
32 YVRDAPV 38

Db

RESULT 35  
F83110  
exodeoxyribonuclease V gamma chain PA4285 [imported] - Pseudomonas aeruginosa (strain PA  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
A:Accession: F83110  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: F83110  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1171 <STO>  
A:Cross-references: UNIPROT:Q9HWB5; GB:AE004844; NID:g9950500; PIDN:AAG0767  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: recC; PA4285  
C:Superfamily: exodeoxyribonuclease V 125K chain

Query Match 77.5%; Score 31; DB 2; Length 1171;  
Best Local Similarity 83.3%; Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YVHDAP 6  
|||  
810 YFHDAP 815

Db

RESULT 36  
A46350  
RNA-directed RNA polymerase (EC 2.7.7.48) - white clover mosaic virus (strain O)  
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase  
C:Species: white clover mosaic virus  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
A:Accession: A46350  
R:Beck, D.L.; Forster, R.L.S.; Bevan, M.W.; Boxen, K.A.; Lowe, S.C.  
Virology 177, 152-158, 1990  
A:Title: Infectious transcripts and nucleotide sequence of cloned cDNA of the potexvirus  
A:Reference number: A46350; MUID:90281578; PMID:2353451  
A:Accession: A46350  
A>Status: translation not shown  
A:Molecule type: genomic RNA  
A:Residues: 1-1293 <BEC>  
A:Cross-references: UNIPROT:P15402; GB:X16636  
C:Superfamily: eggplant mosaic virus RNA-directed RNA polymerase  
C:Keywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA biosynthesis; F  
570-577/Region: nucleotide-binding motif A (P-loop)  
F:633-638/Region: nucleotide-binding motif B  
F:576/Binding site: ATP (lys) #status predicted

Query Match 77.5%; Score 31; DB 1; Length 1293;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YVHDAP 6  
|||  
861 YVHDLP 866

Db

RESULT 37  
S01085  
hypothetical protein 1 - white clover mosaic virus  
C:Species: white clover mosaic virus  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
A:Accession: S01085  
R:Forster, R.L.S.; Bevan, M.W.; Harbison, S.A.; Gardner, R.C.  
Nucleic Acids Res. 16, 291-303, 1988  
A:Title: The complete nucleotide sequence of the potexvirus white clover mosaic virus.  
A:Reference number: S01085; MUID:88124202; PMID:3340527  
A:Accession: S01085  
A:Molecule type: mRNA  
A:Residues: 1-1294 <FOR>  
A:Cross-references: UNIPROT:P09498; EMBL:X06728; NID:g61317; PIDN:CAA29904.1; PID:g6131  
A:Note: 1147-Ala was also found  
C:Superfamily: eggplant mosaic virus RNA-directed RNA polymerase  
C:Keywords: ATP

Query Match 77.5%; Score 31; DB 2; Length 1294;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YVHDAP 6  
|||  
861 YVHDLP 866

Db

RESULT 38  
D69153  
hypothetical protein MTH410 - Methanobacterium thermoautotrophicum (strain Delta H)  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: D69153



R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
i; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierbowski, J.; Gibson, R.; Jiawani, N.  
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcb  
A;Reference number: A69000; MUID:98037514; PMID:9371463  
A;Accession: D69153  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-83 <MTH>  
A;Cross-references: UNIPROT:O26510; GB:AE000825; GB:AE000666; NID:92621465; PIDN:AA88491  
A;Experimental source: strain Delta H  
C;Genetics:  
A;Gene: MTH410

Query Match 75.0%; Score 30; DB 2; Length 83;  
Best Local Similarity 83.3%; Pred. No. 30;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHDAPV 7  
Db 32 VHDSPV 37  
|||:|

RESULT 39  
AH0070  
probable membrane protein YPO0570 [imported] - Yersinia pestis (strain CO92)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AH0070  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Accession: AH0070  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-101 <KUR>  
A;Cross-references: UNIPROT:Q8ZID5; GB:AL590842; PIDN:CAC89427.1; PID:G15978663; GSPDB:G  
C;Genetics:  
A;Gene: YPO0570  
C;Superfamily: conserved hypothetical protein b2672

Query Match 75.0%; Score 30; DB 2; Length 101;  
Best Local Similarity 83.3%; Pred. No. 38;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
Db 75 YVHDNP 80  
|||:|

RESULT 40  
IMECNA  
colicin N immunity protein - Escherichia coli plasmid pCHAP4  
C;Species: Escherichia coli  
C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C;Accession: S01761  
R;Pugsley, A.P.  
Mol. Gen. Genet. 211, 335-341, 1988  
A;Title: The immunity and lysis genes of ColN plasmid pCHAP4.  
A;Reference number: S01760; MUID:88174431; PMID:3280946  
A;Accession: S01761  
A;Molecule type: DNA  
A;Residues: 1-131 <PUG>  
A;Cross-references: UNIPROT:P09182; EMBL:X06933; NID:941117; PIDN:CAA30020.1; PID:G41119  
A;Note: the authors translated the codon ACC for residue 42 as Ile and GTT for residue 1  
C;Genetics:  
A;Gene: cni  
A;Genome: plasmid  
C;Superfamily: colicin N immunity protein

Query Match 75.0%; Score 30; DB 2; Length 164;  
Best Local Similarity 83.3%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
Db 8 YVHSAP 13  
|||:|

RESULT 43  
A41892  
hydrogenase (EC 1.18.99.1) (Nife) b-type cytochrome chain - Rhizobium leguminosarum  
C;Species: Rhizobium leguminosarum  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A41892  
R;Hidalgo, E.; Palacios, J.M.; Murillo, J.; Ruiz-Argueso, T.  
J. Bacteriol. 174, 4130-4139, 1992

C;Keywords: transmembrane protein  
F;66-84/Domain: transmembrane #status predicted <TM1>

Query Match 75.0%; Score 30; DB 1; Length 131;  
Best Local Similarity 71.4%; Pred. No. 50;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7  
Db 33 YVHTAPL 39  
|||:|

RESULT 41  
T38904  
conserved hypothetical protein SPAC56E4.02c - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T38904  
R;Connor, R.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A;Reference number: Z21813  
A;Accession: T38904  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-162 <CON>  
A;Cross-references: UNIPROT:O14190; EMBL:Z99261; PIDN:CAB16393.1; GSPDB:GN00066; SPDB:S  
A;Experimental source: strain 972h-; cosmid c56E4  
C;Genetics:  
A;Gene: SPDB:SPAC56E4.02c  
A;Map position: 1

Query Match 75.0%; Score 30; DB 2; Length 162;  
Best Local Similarity 57.1%; Pred. No. 64;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7  
Db 70 YTHDASI 76  
|||:|

RESULT 42  
T11215  
hypothetical protein 5 - Streptomyces glaucescens  
C;Species: Streptomyces glaucescens  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T11215  
R;Summers, R.G.; Ali, A.; Shen, B.; Wessel, W.A.; Hutchinson, C.R.  
Biochemistry 34, 9389-9402, 1995  
A;Title: Malonyl-coenzyme A:acyl carrier protein acyltransferase of Streptomyces glauc  
A;Reference number: Z17254; MUID:95352622; PMID:7626609  
A;Accession: T11215  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-164 <SUM>  
A;Cross-references: UNIPROT:Q54209; EMBL:L43074; NID:9870805; PID:9870810

Query Match 75.0%; Score 30; DB 2; Length 164;  
Best Local Similarity 83.3%; Pred. No. 65;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
Db 8 YVHSAP 13  
|||:|

RESULT 43  
A41892  
hydrogenase (EC 1.18.99.1) (Nife) b-type cytochrome chain - Rhizobium leguminosarum  
C;Species: Rhizobium leguminosarum  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A41892  
R;Hidalgo, E.; Palacios, J.M.; Murillo, J.; Ruiz-Argueso, T.  
J. Bacteriol. 174, 4130-4139, 1992

A:Title: Nucleotide sequence and characterization of four additional genes of the hydrog  
A:Reference number: A41892; MUID:92283771; PMID:1597428  
A:Accession: A41892  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-239 <HID>  
A:Cross-references: UNIPROT:P27648; GB:X52974; NID:g1167855; PIDN:CAA37150.1; PID:g48723  
A:Experimental source: bv. viciae, UPM791  
A>Note: sequence extracted from NCBI backbone (NCBIN:106282, NCBIP:106285)  
C:Genetics:  
A:Gene: hupC  
C:Superfamily: hycA protein  
C:Keywords: hydrolase; metalloprotein; nickel; oxidoreductase; transmembrane protein  
F:73-89/Domain: transmembrane #status predicted <TM1>  
F:146-162/Domain: transmembrane #status predicted <TM2>  
F:197-213/Domain: transmembrane #status predicted <TM3>

Query Match 75.0%; Score 30; DB 1; Length 239;  
Best Local Similarity 71.4%; Pred. No. 98;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
||:||||  
DB 23 YVYEAPV 29

RESULT 44  
C43255  
hydrogenase (EC 1.18.99.1) (NiFe) b-type cytochrome chain - Alcaligenes eutrophus  
N/Alternate names: hox2 protein  
C:Species: Alcaligenes eutrophus  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: C43255  
R:Kortluke, C.; Horstmann, K.; Schwartz, E.; Rohde, M.; Binsack, R.; Friedrich, B.  
J. Bacteriol. 174, 6277-6289, 1992  
A:Title: A gene complex coding for the membrane-bound hydrogenase of Alcaligenes eutroph  
A:Reference number: A43255; MUID:93015670; PMID:1383192  
A:Accession: C43255  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-244 <KOR>  
A:Cross-references: UNIPROT:P31898; GB:M96433; NID:g141932; PIDN:AAA16463.1; PID:g141935  
A:Experimental source: strain H16, megaplasmid pHG1  
A>Note: sequence extracted from NCBI backbone (NCBIP:115452)  
C:Genetics:  
A:Gene: hox2  
C:Superfamily: hycA protein  
C:Keywords: hydrolase; metalloprotein; nickel; oxidoreductase; transmembrane protein  
F:43-59/Domain: transmembrane #status predicted <TM1>  
F:78-94/Domain: transmembrane #status predicted <TM2>  
F:150-166/Domain: transmembrane #status predicted <TM3>  
F:205-221/Domain: transmembrane #status predicted <TM4>

Query Match 75.0%; Score 30; DB 1; Length 244;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
||:||||  
DB 31 YVYEAPV 37

RESULT 45  
S39400  
hydrogenase (EC 1.18.99.1) (NiFe) b-type cytochrome chain - Bradyrhizobium japonicum  
N/Alternate names: hupC protein  
C:Species: Bradyrhizobium japonicum  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S39400  
R:Van Soom, C.; Browaeys, J.; Verreth, C.; Vanderleyden, J.  
J. Mol. Biol. 234, 508-512, 1993  
A:Title: Nucleotide sequence analysis of four genes, hupC, hupD, hupF and hupG, downstre  
A:Reference number: S39400; MUID:94047099; PMID:8230232

A:Accession: S39400  
A:Molecule type: DNA  
A:Residues: 1-244 <VAN>  
A:Cross-references: UNIPROT:P21960; EMBL:Z21948; NID:g311536; PIDN:CAA79943.1; PID:g3115  
C:Genetics:  
A:Gene: hupC  
C:Superfamily: hycA protein  
C:Keywords: hydrolase; metalloprotein; nickel; oxidoreductase; transmembrane protein  
F:44-60/Domain: transmembrane #status predicted <TM1>  
F:87-103/Domain: transmembrane #status predicted <TM2>  
F:155-171/Domain: transmembrane #status predicted <TM3>  
F:205-221/Domain: transmembrane #status predicted <TM4>

Query Match 75.0%; Score 30; DB 1; Length 244;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
||:||||  
DB 32 YVYEAPV 38

RESULT 46  
F87242  
probable secreted protein [imported] - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: F87242  
R:Cole, S.T.; Biglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holroyd,  
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,  
eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S.  
A:Title: Massive gene decay in the leprosy bacillus.  
A:Reference number: A86909; MUID:21128732; PMID:11234002  
A:Accession: F87242  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-251 <STO>  
A:Cross-references: UNIPROT:Q9ZBE6; GB:AL450380; NID:g13093866; PIDN:CAC32196.1; GSPDB:  
C:Genetics:  
A:Gene: ML2664

Query Match 75.0%; Score 30; DB 2; Length 251;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAVP 6  
||:||||  
DB 206 YVHSAP 211

RESULT 47  
G70840  
hypothetical protein Rv0116c - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: G70840  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Sqaes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: G70840  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-251 <COL>  
A:Cross-references: UNIPROT:O53638; GB:AL021926; GB:AL123456; NID:g3261520; PIDN:CAA1731  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv0116c

Query Match 75.0%; Score 30; DB 2; Length 251;  
Best Local Similarity 83.3%; Pred. No. 1.e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|||  
Db 206 YVHSAP 211

RESULT 48  
D70915  
hypothetical protein Rv1433 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: D70915  
R:Cole, S.T.; Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Byles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: D70915  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-271 <COL>  
A:Cross-references: UNIPROT:O06825; GB:Z95844; GB:AL123456; NID:g3250713; PIDN:CAB09251  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: Rv1433

Query Match 75.0%; Score 30; DB 2; Length 271;  
Best Local Similarity 83.3%; Pred. No. 1.e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|||  
Db 226 YVHSAP 231

RESULT 49  
D69881  
yabC protein homolog ylxA - Bacillus subtilis  
N:Alternate names: pbbP 5'-region hypothetical protein B  
C:Species: Bacillus subtilis  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: D69881; A53292  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.  
Koether, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377  
A:Accession: D69881  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-311 <KUN>  
A:Cross-references: UNIPROT:Q07876; GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13387  
A:Experimental source: strain 168  
R:Yanouri, A.; Daniel, R.A.; Errington, J.; Buchanan, C.E.  
J. Bacteriol. 175, 7604-7616, 1993  
A:Title: Cloning and sequencing of the cell division gene pbbB, which encodes penicillin

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|  
Db 71 YLHKAPV 77

RESULT 52  
E82168  
probable alpha-1,6-galactosidase VC1690 [imported] - Vibrio cholerae (strain N16961 sero  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: E82168  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F  
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: E82168  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-374 <HEI>  
A;Cross-references: UNIPROT:Q9KR2; GB:AE004247; GB:AE003852; NID:g9656204; PIDN:AAF9484  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC1690  
A;Map position: 1

Query Match 75.0%; Score 30; DB 2; Length 374;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|  
Db 93 YPHDAP 98

RESULT 53  
B83242  
hypothetical protein PA3238 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: B83242  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: B83242  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-453 <STO>  
A;Cross-references: UNIPROT:Q9HZ02; GB:AE004745; GB:AE004091; NID:g9949350; PIDN:AAG0662  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA3238

Query Match 75.0%; Score 30; DB 2; Length 453;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|  
Db 373 YLHDSP 378

RESULT 54  
S16727  
coenzyme F420 hydrogenase (EC 1.12.99.1) alpha chain vhcA [similarity] - Methanococcus v  
C;Species: Methanococcus voltae  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S16727; S32835  
R;Halboth, S.; Klein, A.  
submitted to the EMBL Data Library, August 1991  
A;Description: Methanococcus voltae harbors two gene groups each of homologous (Nife) - a  
A;Reference number: S16721  
A;Accession: S16727  
A;Molecule type: DNA  
A;Residues: 1-474 <HAL>  
A;Cross-references: UNIPROT:Q00404; EMBL:X61203; NID:g296614; PIDN:CAA43506.1; PID:g4479  
A;Experimental source: strain PS (DSM1537)  
R;Halboth, S.; Klein, A.  
Mol. Gen. Genet. 233, 217-224, 1992  
A;Title: Methanococcus voltae harbors four gene clusters potentially encoding two [Nife]  
A;Reference number: A59304; MUID:92293118; PMID:1603063  
A;Contents: annotation  
C;Genetics:  
A;Gene: vhcA  
C;Superfamily: methyl viologen-reducing hydrogenase alpha chain  
C;Keywords: oxidoreductase

Query Match 75.0%; Score 30; DB 2; Length 474;  
Best Local Similarity 57.1%; Pred. No. 2.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|  
Db 49 YIEDAPI 55

RESULT 55  
AF2206  
Glutaryl-tRNA synthetase [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AF2206  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete genomic sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AF2206  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-480 <KUR>  
A;Cross-references: UNIPROT:Q8Y886; GB:BA000019; PIDN:BAE74904.1; PID:g17132300; GSPDB:  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: gltX  
C;Superfamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

Query Match 75.0%; Score 30; DB 2; Length 480;  
Best Local Similarity 57.1%; Pred. No. 2.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|  
Db 322 YIHNTPV 328

RESULT 56  
G70941  
hypothetical protein Rv2024c - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: G70941  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: G70941  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-515 <COL>  
A;Cross-references: UNIPROT:O53470; GB:AL021899; GB:AL123456; NID:G3242282; PIDN:CAA1723  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: RV2024c

Query Match 75.0%; Score 30; DB 2; Length 515;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7  
:|||||:  
Db 265 HVHDVPI 271

RESULT 57  
AD1216  
ABC transporters, ATP-binding proteins homolog lmo1132 [imported] - *Listeria monocytogenes*  
C;Species: *Listeria monocytogenes*  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AD1216  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AD1216  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-548 <GLA>  
A;Cross-references: UNIPROT:Q8V7Y7; GB:NC\_003210; PIDN:CAC99210.1; PID:gl616410548; GSPDB:  
A;Experimental source: strain EGD-e  
C;Genetics:  
A;Gene: lmo1132  
C;Superfamily: Mycobacterium tuberculosis probable ABC transporter cydC; ATP-binding cas

Query Match 75.0%; Score 30; DB 2; Length 548;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7  
:|||||:  
Db 482 FLHDAPL 488

RESULT 58  
A11569  
ABC transporters, ATP-binding protein homolog lin1098 [imported] - *Listeria innocua* (str  
C;Species: *Listeria innocua*  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: A11569  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Krest, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: A11569  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-548 <GLA>  
A;Cross-references: UNIPROT:Q92CS3; GB:AL592022; PIDN:CAC96329.1; PID:gl616413557; GSPDB:G  
A;Experimental source: strain Clip11262  
C;Genetics:  
A;Gene: lin1098

Query Match 75.0%; Score 30; DB 2; Length 548;  
Best Local Similarity 57.1%; Pred. No. 2.4e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7  
:|||||:  
Db 482 FLHDAPL 488

## RESULT 59

I51368  
gamma-aminobutyric acid transport protein GAT-1 - Pacific electric ray  
C;Species: *Torpedo californica* (Pacific electric ray)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I51368; S42808  
R;Swanson, G.T.; Umbach, J.A.; Gundersen, C.B.  
J. Neurochem. 63, 1-12, 1994  
A;Title: Glia of the cholinergic electromotor nucleus of Torpedo are the source of the  
A;Reference number: I51368; MUID:94267441; PMID:8207419  
A;Accession: I51368  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-598 <SWA>  
A;Cross-references: UNIPROT:Q91494; EMBL:X77139; NID:G444009; PIDN:CAA54394.1; PID:G444  
C;Genetics:  
A;Gene: TGAT-1  
C;Superfamily: gamma-aminobutyric acid transporter

Query Match 75.0%; Score 30; DB 2; Length 598;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHDAPV 7  
:|||||:  
Db 17 LHDAPV 22

## RESULT 60

T20714  
hypothetical protein F10F2.7 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T20714  
R;Coles, L.  
submitted to the EMBL Data Library, August 1994  
A;Reference number: Z19313  
A;Accession: T20714  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-628 <WIL>  
A;Cross-references: UNIPROT:Q19313; EMBL:Z35598; PIDN:CAA84652.1; GSPDB:GNO0021; CESP:F  
C;Genetics:  
A;Gene: CESP:F10F2.7  
A;Map position: 3  
A;Introns: 82/3; 100/3; 187/1; 368/3; 403/2; 491/1

Query Match 75.0%; Score 30; DB 2; Length 628;  
Best Local Similarity 71.4%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7  
:|||||:  
Db 455 YVHGAPL 461

## RESULT 61

AG2020  
DNA ligase [imported] - *Nostoc* sp. (strain PCC 7120)  
C;Species: *Nostoc* sp. PCC 7120  
A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 12-Jul-2004

C:Accession: AG2020  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG2020  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-677 <KUR>  
A:Cross-references: UNIPROT:Q8Y9W8; GB:BA000019; PIDN:BAH78083.1; PID:gl17135537; GSPDB:G000000001  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all1717  
C:Superfamily: NAD+-dependent DNA ligase, LigA type

Query Match 75.0%; Score 30; DB 2; Length 677;  
Best Local Similarity 71.4%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
Db 26 YVSDAPI 32

RESULT 62  
B56277  
DNA-directed DNA polymerase (EC 2.7.7.7) II - Pyrodicticum occultum  
C:Species: Pyrodicticum occultum  
C:Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
C:Accession: B56277  
R;Umori, T.; Ishino, Y.; Doi, H.; Kato, I. J. Bacteriol. 177, 2164-2177, 1995  
A:Title: The hyperthermophilic archaeon Pyrodicticum occultum has two alpha-like DNA polymerases  
A:Reference number: A56277; MUID:95238290; PMID:7721707  
A:Accession: B56277  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-803 <UEM>  
A:Cross-references: UNIPROT:Q59691; GB:D38574; NID:G807829; PIDN:BAA07580.1; PID:G807830  
C:Superfamily: DNA polymerase  
C:Keywords: nucleotidyltransferase

Query Match 75.0%; Score 30; DB 2; Length 803;  
Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|||  
Db 705 YEHDP 710

RESULT 63  
S62136  
CW41 protein - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein G3664; protein YGL027c  
C:Species: Saccharomyces cerevisiae  
C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: S62136; S64029; JG6020  
R;Jiang, B.; Sheraton, J.; Ram, A.F.J.; Dijkgraaf, G.J.P.; Klis, F.M.; Bussey, H. J. Bacteriol. 178, 1162-1171, 1996  
A:Title: CW41 encodes a novel endoplasmic reticulum membrane N-glycoprotein involved in protein translocation  
A:Reference number: S62136; MUID:96165274; PMID:8576053  
A:Accession: S62136  
A:Molecule type: DNA  
A:Residues: 1-833 <JIA>  
A:Cross-references: UNIPROT:P53008; EMBL:U35669; NID:g1176412; PIDN:AAC49157.1; PID:g1176412  
A:Experimental source: cell wall  
R;Hebling, U.; Hofmann, B.; Delius, H. submitted to the Protein Sequence Database, May 1996  
A:Reference number: S64003  
A:Accession: S64029  
A:Molecule type: DNA

C:Accession: AG2020  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AG2020  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-677 <KUR>  
A:Cross-references: UNIPROT:Q8Y9W8; GB:BA000019; PIDN:BAH78083.1; PID:gl17135537; GSPDB:G000000001  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all1717  
C:Superfamily: NAD+-dependent DNA ligase, LigA type

Query Match 75.0%; Score 30; DB 2; Length 833;  
Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
Db 62 YVHESPL 68

RESULT 64  
A38172  
adenylate cyclase (EC 4.6.1.1) - Pasteurella multocida  
C:Species: Pasteurella multocida  
C:Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: A38172  
R;Mock, M.; Cranier, M.; Duflot, E.; Dumay, V.; Danchin, A. J. Bacteriol. 173, 6265-6269, 1991  
A:Title: Structural and functional relationships between Pasteurella multocida and enteric adenylate cyclase  
A:Reference number: A38172; MUID:92011391; PMID:1917858  
A:Accession: A38172  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-838 <MOC>  
A:Cross-references: UNIPROT:Q05766; GB:M68901; NID:gi50497; PIDN:AAA25532.1; PID:g551912  
C:Superfamily: adenylate cyclase  
C:Keywords: phosphorus-oxygen lyase

Query Match 75.0%; Score 30; DB 2; Length 838;  
Best Local Similarity 85.7%; Pred. No. 3.9e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||  
Db 52 YVADAPV 58

RESULT 65  
AB0539  
Rhs-family protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain 14028)  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AB0539  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, P.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001  
A:Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davies, P.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AB0539  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-843 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD08754.1; PID:gi6501575; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY0324

Query Match 75.0%; Score 30; DB 2; Length 843;

Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YVHDAP 6  
|:|:|  
Db 647 YVYDAP 652

RESULT 66  
T00491  
capsid protein precursor - himetobi p virus (fragment)  
C;Species: himetobi p virus  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T00491  
R;Nakashima, N.; Sasaki, J.  
submitted to the EMBL Data Library, August 1998  
A;Description: Complete nucleotide sequence of an insect picorna-like virus, Himetobi p  
A;Reference number: Z14156  
A;Accession: T00491  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-874 <NAK>  
A;Cross-references: UNIPROT:O89279; EMBL:AB017037; NID:d1226972; PIDN:BAA32554.1; PID:d1226972  
C;Keywords: capsid protein

Query Match 75.0%; Score 30; DB 2; Length 874;  
Best Local Similarity 66.7%; Pred. No. 4.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YVHDAP 6  
|:|:|  
Db 737 YIHDLP 742

RESULT 67  
AE0418  
valine-tRNA ligase (EC 6.1.1.9) [imported] - Yersinia pestis (strain C092)  
C;Species: Yersinia pestis  
C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AE0418  
R;Parthill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Accession: AE0418  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-965 <KUR>  
A;Cross-references: UNIPROT:Q82BH1; GB:AL590842; PIDN:CAC92673.1; PID:gl5981369; GSPDB:G  
C;Genetics:  
A;Gene: valS  
C;Superfamily: valine-tRNA ligase  
C;Keywords: ligase

Query Match 75.0%; Score 30; DB 2; Length 965;  
Best Local Similarity 71.4%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YVHDAP 7  
|:|:|  
Db 397 YVHTAPL 403

RESULT 68  
A64828  
cell division protein ftsK - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: A64828  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: A64828  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1329 <BLAT>  
A;Cross-references: UNIPROT:P46889; GB:AE000191; GB:U00096; NID:gl787115; PIDN:AAC73976  
A;Experimental source: strain K-12, substrain MG1655  
C;Genetics:  
A;Gene: ftsK  
C;Function:  
A;Description: may act late the in septation process  
C;Keywords: ATP; cell division; nucleotide binding; P-loop; transmembrane protein  
F;26-42/Domain: transmembrane #status predicted <TM1>  
F;75-91/Domain: transmembrane #status predicted <TM2>  
F;116-132/Domain: transmembrane #status predicted <TM3>  
F;162-178/Domain: transmembrane #status predicted <TM4>  
F;560-576/Domain: transmembrane #status predicted <TM5>  
F;991-998/Region: nucleotide-binding motif A (P-loop)

Query Match 75.0%; Score 30; DB 2; Length 1329;  
Best Local Similarity 71.4%; Pred. No. 6.5e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
|:|:|  
Db 667 YQHDVPV 673

RESULT 69  
E85614  
cell division protein ftsK [imported] - Escherichia coli (strain O157:H7, substrain EDL  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C;Accession: E85614  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayh  
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: E85614  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1342 <STO>  
A;Cross-references: GB:AE005174; NID:gl2514052; PIDN:AAG55377.1; GSPDB:GN00145; UWGP:Z  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: ftsK

Query Match 75.0%; Score 30; DB 2; Length 1342;  
Best Local Similarity 71.4%; Pred. No. 6.6e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YVHDAPV 7  
|:|:|  
Db 667 YQHDVPV 673

RESULT 70  
G90750  
cell division protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: G90750  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G  
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A;Reference number: A9629; MUID:21156231; PMID:11258796  
A;Accession: G90750  
A;Status: preliminary  
A;Molecule type: DNA

A;Residues: 1-1342 <HAY>  
A;Cross-references: UNIPROT:Q8XSH9; GB:BA000007; PIDN:BA834398.1; PID:gl3360434; GSPDB:G  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: ECs0975

Query Match 75.0%; Score 30; DB 2; Length 1342;  
Best Local Similarity 71.4%; Pred. No. 6.6e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 667 YQHDVPEV 673

RESULT 71  
UPRCX  
D-Xylose uptake protein - Escherichia coli  
C;Species: Escherichia coli  
C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C;Accession: A24334  
R;Kurose, N.; Watanabe, K.; Kimura, A.  
Nucleic Acids Res. 14, 7115-7123, 1986  
A;Title: Nucleotide sequence of the gene responsible for D-xylose uptake in Escherichia  
A;Reference number: A24334; MUID:87016348; PMID:3532033  
A;Accession: A24334  
A;Molecule type: DNA  
A;Residues: 1-61 <KUR>  
A;Cross-references: UNIPROT:P05056; GB:X04387; NID:g43317; PIDN:CAA27976.1; PID:g43318  
C;Comment: This protein enables E. coli mutants to recover from a decrease in D-xylose u  
C;Genetics:  
A;Map position: 80 min  
C;Superfamily: D-xylose uptake protein  
C;Keywords: xylose transport

Query Match 72.5%; Score 29; DB 1; Length 61;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
| | | | |  
Db 12 VHDAP 16

RESULT 72  
E69464  
hypothetical protein AF1718 - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: E69464  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: E69464  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-66 <KLE>  
A;Cross-references: UNIPROT:O28556; GB:AE000985; NID:g2689308; PIDN:AAB8954

Query Match 72.5%; Score 29; DB 2; Length 66;  
Best Local Similarity 57.1%; Pred. No. 38;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 47 YTHEADL 53

## RESULT 73

T09540  
proline rich protein, auxin-induced - alfalfa  
C;Species: Medicago sativa (alfalfa)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T09540  
R;Gyorgyev, J.; Nemeth, K.; Magyar, Z.; Alliotte, T.; Inze, D.; Dudits, D.  
Submitted to the EMBL Data Library, July 1996  
A;Description: Expression of a novel type small proline rich protein is induced by auxin  
A;Reference number: Z16727  
A;Accession: T09540  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-84 <GVO>  
A;Cross-references: UNIPROT:O24072; EMBL:X99099; NID:e996303; PID:e255370  
A;Experimental source: strain RA3; callus  
C;Superfamily: proline-rich protein 3

Query Match 72.5%; Score 29; DB 2; Length 84;  
Best Local Similarity 57.1%; Pred. No. 50;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
| | | | |  
Db 28 YIHSTPV 34

## RESULT 74

G87460  
hypothetical protein CC1707 [imported] - Caulobacter crescentus  
C;Species: Caulobacter crescentus  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C;Accession: G87460  
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A;Title: Complete Genome Sequence of Caulobacter crescentus.  
A;Reference number: A87249; MUID:21173698; PMID:11255967  
A;Accession: G87460  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-117 <STO>  
A;Cross-references: UNIPROT:Q9A7L5; GB:AE005673; NID:gl3423121; PIDN:AAK23683.1; GSPDB:G  
C;Genetics:  
A;Gene: CC1707

Query Match 72.5%; Score 29; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAPV 7  
| | | | |  
Db 59 HDAPV 63

## RESULT 75

F83297  
hypothetical protein PA2790 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: F83297  
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: F83297  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-161 <STO>  
A;Cross-references: UNIPROT:Q91053; GB:AE004706; GB:AE004091; NID:g9948864; PIDN:AAG061



A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA2790

Query Match 72.5%; Score 29; DB 2; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAPV 7  
| | | | |  
Db 149 HDAPV 153

## RESULT 76

S56944

N;Alternate names: hypothetical protein YJL161w - yeast (*Saccharomyces cerevisiae*)

C;Species: *Saccharomyces cerevisiae*

C;Date: 08-Jul-1995 #sequence\_revision 08-Sep-1995 #text\_change 09-Jul-2004

C;Accession: S56944

R;Obermaier, B.; Piravandi, E.; Rinke, M.; Domdey, H.

submitted to the Protein Sequence Database, September 1995

A;Reference number: S56937

A;Accession: S56944

A;Molecule type: DNA

A;Residues: 1-180 <OBE>

A;Cross-references: UNIPROT:P46998; EMBL:Z49436; NID:g1008345; PID:g1008346; GSPDB:GN000

C;Genetics:

A;Gene: MIPS:YJL161w

A;Cross-references: SGD:S0003697

A;Map position: 10L

C;Superfamily: *Saccharomyces* probable membrane protein YJL161w

C;Keywords: transmembrane protein

Query Match 72.5%; Score 29; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
| | | | |  
Db 79 VHDAP 83

## RESULT 77

A84347

hypothetical protein Vng1962c [imported] - *Halobacterium* sp. NRC-1

C;Species: *Halobacterium* sp. NRC-1

C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C;Accession: A84347

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laskey, S.

; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A;Title: Genome sequence of *Halobacterium* species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84347

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-180 <STO>

A;Cross-references: UNIPROT:Q9HNS9; GB:AE004437; NID:g10581398; PIDN:AAG20141.1; GSPDB:G

C;Genetics:

A;Gene: VNG1962C

Query Match 72.5%; Score 29; DB 2; Length 180;

Best Local Similarity 66.7%; Pred. No. 1.2e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
Db 41 YLHDGP 46

## RESULT 78

F97499

hypothetical protein AGR\_C\_2123 [imported] - *Agrobacterium tumefaciens* (strain C58, Cer

C;Species: *Agrobacterium tumefaciens*

C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004

C;Accession: F97499

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman

A.; Liu, F.; Woilam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium* tu

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: F97499

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-182 <KUR>

A;Cross-references: UNIPROT:Q8UG92; GB:AE007869; PIDN:AAK86951.1; PID:g15156185; GSPDB:

C;Genetics:

A;Gene: AGR\_C\_2123

A;Map position: circular chromosome

Query Match 72.5%; Score 29; DB 2; Length 182;

Best Local Similarity 83.3%; Pred. No. 1.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
Db 11 YVHDGP 16

## RESULT 79

H70726

probable holliday junction dna helicase - *Mycobacterium tuberculosis* (strain H37RV)

C;Species: *Mycobacterium tuberculosis*

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C;Accession: H70726

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: H70726

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-196 <COL>

A;Cross-references: UNIPROT:Q50628; GB:Z77724; GB:AL123456; NID:g3261620; PIDN:CAB01282

A;Experimental source: strain H37RV

C;Genetics:

A;Gene: ruva

C;Superfamily: holliday junction DNA helicase ruva

Query Match 72.5%; Score 29; DB 2; Length 196;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
| | | | |  
Db 91 VHDAP 95

## RESULT 80

T22344

hypothetical protein F47B8.6 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T22344

R;Berks, M.; McMurray, A.

submitted to the EMBL Data Library, July 1996

A;Reference number: Z19551

A;Accession: T22344

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-210 <WIL>  
A;Cross-references: UNIPROT:Q20520; EMBL:Z77662; PIDN:CAB01195.1; GSPDB:GN00023; CESP:F47B8  
A;Experimental source: clone F47B8  
C;Genetics:  
A;Gene: CESP:F47B8.6  
A;Map position: 5  
A;Introns: 71/1, 172/3

Query Match 72.5%; Score 29; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDA 5  
|||

DB 79 YVHDA 83

## RESULT 81

A47581 septal cell wall dissolution factor spoIIM - Bacillus subtilis  
N;Alternate names: sporulation protein spoIIM  
C;Species: Bacillus subtilis  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C;Accession: A47581; H69712  
R;Smith, K.; Bayer, M.E.; Youngman, P.  
J. Bacteriol. 175, 3607-3617, 1993  
A;Title: Physical and functional characterization of the Bacillus subtilis spoIIM gene.  
A;Reference number: A47581; MUID:93273731; PMID:8501064

A;Accession: A47581  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-214 <SMI>  
A;Cross-references: UNIPROT:P37873; GB:I06664; NID:G143633; PIDN:AAA5553.1; PID:G143634  
R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, C.; Brun, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chao, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogasawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yaumoto, K.; Yata, K.; Yoshida, K. A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: H69712  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-214 <KUN>  
A;Cross-references: GB:Z99116; GB:AL009126; NID:G2634723; PIDN:CAB14285.1; PID:e1185622;  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: spoIIM

Query Match 72.5%; Score 29; DB 2; Length 214;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
:|||||

DB 169 LHDAPV 174

## RESULT 82

T16559 hypothetical protein K04E7.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T16559

R;Nhan, M.  
submitted to the EMBL Data Library, October 1995  
A;Description: The sequence of C. elegans cosmid K04E7.  
A;Reference number: Z18535  
A;Accession: T16559  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-217 <NHA>  
A;Cross-references: UNIPROT:Q21220; EMBL:U39666; NID:G1049408; PID:G1049409; PIDN:AAA804  
A;Experimental source: strain Bristol N2  
C;Genetics:  
A;Gene: CESP:K04E7.1  
A;Introns: 65/1, 139/3, 172/3

Query Match 72.5%; Score 29; DB 2; Length 217;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
:|||||

DB 186 LHDAPV 191

## RESULT 83

T30415 host range factor 1 - Lymantria dispar nuclear polyhedrosis virus  
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30415  
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr, A.; Titley, S.; 17-34, 1999  
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria  
A;Reference number: Z20836; MUID:99124785; PMID:9887315  
A;Accession: T30415  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-218 <KUZ>  
A;Cross-references: UNIPROT:Q90165; EMBL:AF081810; NID:G3822234; PIDN:AAC70253.1; PID:G3  
C;Superfamily: Lymantria dispar nuclear polyhedrosis virus host range factor 1

Query Match 72.5%; Score 29; DB 2; Length 218;  
Best Local Similarity 57.1%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|||

DB 108 YAHDGPL 114

## RESULT 84

F83131 conserved hypothetical protein PA4121 [imported] - Pseudomonas aeruginosa (strain PA01)  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: F83131  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: F83131  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-219 <STO>  
A;Cross-references: UNIPROT:Q9HWR0; GB:AE004828; GB:AE004091; NID:G9950315; PIDN:AAG0751  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA4121

Query Match 72.5%; Score 29; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HDAPV 7  
|:|:|:|  
Db 56 HDAPV 60

## RESULT 85

E70039  
glycolate oxidase homolog yvfV - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: E70039  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertsch, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd C.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Levine, A.; Liu, H.; Masuda, S.; Maueel Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A;Title: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: E70039  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-238 <XUN>  
A;Cross-references: UNIPROT:O07020; GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15410.  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: yvfV  
C;Superfamily: conserved hypothetical protein HP0139

Query Match 72.5%; Score 29; DB 2; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YHDA 5  
|:|:|:|  
Db 51 YHDA 55

## RESULT 86

AB0676  
Ni/Fe-hydrogenase 1 b-type cytochrome chain HyaC2 [imported] - Salmonella enterica subsp C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AB0676  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001.  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AB0676  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-242 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD01779.1; PID:g16502625; GSPDB:GN00176  
C;Genetics:  
A;Gene: hyaC2  
C;Superfamily: hyaC protein

Query Match 72.5%; Score 29; DB 2; Length 242;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|:|  
Db 30 YIVEAPV 36

## RESULT 87

JC5237  
osmotin-like protein precursor - tomato  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: JC5237  
R;Chen, R.; Wang, F.; Smith, A.G. Gene 179, 301-302, 1996  
A;Title: A flower-specific gene encoding an osmotin-like protein from Lycopersicon escul A;Reference number: JC5237; MUID:97128324; PMID:8972917  
A;Contents: flower  
A;Accession: JC5237  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-252 <CHE>  
A;Cross-references: UNIPROT:Q41350; GB:L76632; NID:g1220536; PIDN:AAB41124.1; PID:g1220 C;Comment: This protein is rich in cysteine content and play a part of the flowers defe C;Superfamily: thaumatin I  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-252/Product: osmotin-like protein #status predicted <MAT>

Query Match 72.5%; Score 29; DB 2; Length 252;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
|:|:|:|  
Db 229 YAHDSP 234

## RESULT 88

PMYCA6  
H+-transporting two-sector ATPase (EC 3.6.3.14) chain a - Synechococcus sp. (strain PCC N;Alternate names: H+-transporting ATP synthase protein 6  
C;Species: Synechococcus sp.  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: S10826  
R;Cozens, A.L.; Walker, J.E. J. Mol. Biol. 194, 359-383, 1987  
A;Title: The organization and sequence of the genes for ATP synthase subunits in the cy A;Reference number: S07286; MUID:87311713; PMID:3041005  
A;Accession: S10826  
A;Molecule type: DNA  
A;Residues: 1-261 <COZ>  
A;Cross-references: UNIPROT:P08444; EMBL:X05302; NID:g48009; PIDN:CAA28923.1; PID:g4801 C;Superfamily: H+-transporting ATP synthase protein 6  
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; transmembrane pro

Query Match 72.5%; Score 29; DB 1; Length 261;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|:|  
Db 173 YVHPTPV 179

## RESULT 89

AE3545  
dipeptide transport system permease protein dppC [imported] - Brucella melitensis (stra C;Species: Brucella melitensis  
C;Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C;Accession: AE3545  
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, ; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leter Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten

A:Reference number: AD3252; PMID:11756688

A:Accession: AE3545

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-264 <KUR>

A:Cross-references: UNIPROT:Q8YD91; GB:AE008918; PIDN:AAL53528.1; PID:gl7984435; GSPDB:G

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEII0286

A:Map position: II

C:Superfamily: oligopeptide permease protein oppB

Query Match 72.5%; Score 29; DB 2; Length 264;

Best Local Similarity 66.7%; Pred. No. 1.8e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6

|||||

Db 223 YIYDAP 228

RESULT 90

S72782

B1496\_F2.81 protein - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S72782

R:Smith, D.R.; Robinson, K.

A:Submitted to the EMBL Data Library, November 1993

A:Description: Mycobacterium leprae cosmid B1496.

A:Reference number: S72695

A:Accession: S72782

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-271 <SMI>

A:Cross-references: UNIPROT:Q49706; EMBL:U00013; NID:g466869; PIDN:AAAL7146.1; PID:g4669

Query Match 72.5%; Score 29; DB 2; Length 271;

Best Local Similarity 66.7%; Pred. No. 1.8e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6

|||||

Db 226 YIHSAP 231

RESULT 91

T17629

Hypothetical protein A138R - Chlorella virus PBCV-1

C:Species: Chlorella virus PBCV-1

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T17629

R:Graves, M.V.; Van Etten, J.L.

A:Submitted to the EMBL Data Library, May 1999

A:Reference number: Z1806

A:Accession: T17629

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-273 <GRA>

A:Cross-references: UNIPROT:Q84458; EMBL:U42580; NID:g4028896; PIDN:AAC96506.1

A:Experimental source: specific host Chlorella strain NC64A

C:Genetics:

A:Note: A138R

C:Superfamily: Chlorella virus PBCV-1 hypothetical protein A138R

Query Match 72.5%; Score 29; DB 2; Length 273;

Best Local Similarity 66.7%; Pred. No. 1.8e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6

|||||

Db 193 YIYDAP 198

RESULT 92

F83923

manganese-containing catalase BH2190 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C:Accession: F83923

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: F83923

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-281 <STO>

A:Cross-references: UNIPROT:Q9KAU6; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BA0059

A:Experimental source: strain C-125

C:Genetics:

A:Gene: BH2190

Query Match 72.5%; Score 29; DB 2; Length 281;

Best Local Similarity 42.9%; Pred. No. 1.9e+02;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7

|||||

Db 265 YIHVTPI 271

RESULT 93

P8ECAL

phospholipase A1 (EC 3.1.1.32) precursor - Escherichia coli (strain K-12)

N:Alternate names: outer-membrane phospholipase A; phosphatidylcholine 1-acylhydrolase;

C:Species: Escherichia coli

C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 09-Jul-2004

C:Accession: A22133; S30711; A00771; S66447; F65186

R:Homma, H.; Kobayashi, T.; Chiba, N.; Karasawa, K.; Mizushima, H.; Kudo, I.; Inoue, K.;

J. Biochem. 96, 1655-1664, 1984

A:Title: The DNA sequence encoding pldA gene, the structural gene for detergent-resistat

A:Reference number: A22133; MUID:85157492; PMID:6397464

A:Accession: A22133

A:Molecule type: DNA

A:Residues: 1-289 <HOM>

A:Cross-references: UNIPROT:P00631; GB:X02143; GB:X00780; NID:g42423; PIDN:CAA26081.1; I

A:Note: this enzyme is tightly bound to the outer membrane of the cell

R:Danielis, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.

Science 257, 771-778, 1992

A:Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 t

A:Reference number: S30660; MUID:92358234; PMID:1379743

A:Accession: S30711

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-13, 'FA', 16-289 <DAN>

A:Cross-references: EMBL:M87049; NID:9836656; PIDN:AAA67617.1; PID:gl48220

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992

R:de Geus, P.; Verheij, H.M.; Riegman, N.H.; Hoekstra, W.P.M.; de Haas, G.H.

EMBO J. 3, 1799-1802, 1984

A:Title: The pro- and mature forms of the E. coli K-12 outer membrane phospholipase A.

A:Reference number: A00771; MUID:85003590; PMID:6383820

A:Accession: A00771

A:Molecule type: DNA

A:Residues: 'MTRQ', 34-289 <DEG>

R:Dekker, N.; Merck, K.; Tommassen, J.; Verheij, H.M.

Eur. J. Biochem. 232, 214-219, 1995

A:Title: In vitro folding of Escherichia coli outer-membrane phospholipase A.

A:Reference number: S66447; MUID:96048049; PMID:7556153

A:Accession: S66447

A>Status: preliminary

A:Molecule type: protein

A:Residues: 21-24 <DEK>

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli* K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: F65186  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-289 <BLAT>  
A;Cross-references: GB:AE000458; GB:U00096; NID:G2367299; PIDN:NACT6824.1; PID:G2367300;  
A;Experimental source: strain K-12, substrain MG1655  
C;Comment: This enzyme is tightly bound to the outer membrane of the cell.  
C;Genetics:  
A;Gene: pldA  
A;Map position: 85 min  
C;Superfamily: bacterial phospholipase A1  
F;Keywords: carboxylic ester hydrolase; membrane bound  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-289/Product: phospholipase A1 #status predicted <MPT>

Query Match 72.5%; Score 29; DB 1; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
|||||  
Db 28 VHDAP 32

RESULT 94  
AI0917  
detergent-resistant phospholipase A [imported] - *Salmonella enterica* subsp. *enterica* ser  
C;Species: *Salmonella enterica* subsp. *enterica* serovar Typhi  
A;Note: this species has also been called *Salmonella typhi*  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AI0917  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AI0917  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-289 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD07935.1; PID:G16504480; GSPDB:GN00176  
C;Genetics:  
A;Gene: STY3602  
C;Superfamily: bacterial phospholipase A1

Query Match 72.5%; Score 29; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
|||||  
Db 28 VHDAP 32

RESULT 95  
E86069  
outer membrane phospholipase A [imported] - *Escherichia coli* (strain O157:H7, substrain  
C;Species: *Escherichia coli*  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: E86069  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: E86069  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-289 <STO>

A;Cross-references: UNIPROT:P00631; GB:AE005174; NID:G12518695; PIDN:AAGS9017.1; GSPDB:  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: pldA  
C;Superfamily: bacterial phospholipase A1

Query Match 72.5%; Score 29; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
|||||  
Db 28 VHDAP 32

RESULT 96  
G91222  
outer membrane phospholipase A ECs4751 [imported] - *Escherichia coli* (strain O157:H7, s  
C;Species: *Escherichia coli*  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: G91222  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gen  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: G91222  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-289 <HAY>  
A;Cross-references: UNIPROT:P00631; GB:BA000007; PIDN:BA838174.1; PID:G13364227; GSPDB:  
A;Experimental source: strain O157:H7, substrain RMD 0509952  
C;Genetics:  
A;Gene: ECs4751  
C;Superfamily: bacterial phospholipase A1

Query Match 72.5%; Score 29; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
|||||  
Db 28 VHDAP 32

RESULT 97  
A36971  
outer membrane phospholipase A (EC 3.1.1.1.-) precursor - *Salmonella typhimurium*  
C;Species: *Salmonella typhimurium*  
C;Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A36971; S40131  
R;Brok, R.G.P.M.; Brinkman, E.; van Bortel, R.; Bekkers, A.C.A.P.A.; Verheij, H.M.; Tom  
J. Bacteriol. 176, 861-870, 1994  
A;Title: Molecular characterization of enterobacterial pldA genes encoding outer membra  
A;Reference number: A36971; MUID:94131966; PMID:8300539  
A;Accession: A36971  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-289 <BRO>  
A;Cross-references: UNIPROT:P37442; GB:X76900; NID:G437024; PIDN:CAAS4222.1; PID:G43702  
C;Genetics:  
A;Gene: pldA  
C;Superfamily: bacterial phospholipase A1  
C;Keywords: carboxylic ester hydrolase

Query Match 72.5%; Score 29; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
|||||  
Db 28 VHDAP 32

## RESULT 98

KIOXPR  
phosphoribulokinase (EC 2.7.1.19) - Xanthobacter flavus  
C:Species: Xanthobacter flavus  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: B45867; S13577  
R:Meijer, W.G.; Enequist, H.G.; Terpstra, P.; Dijkhuizen, L.  
J. Gen. Microbiol. 136, 2225-2230, 1990  
A:Title: Nucleotide sequences of the genes encoding fructosebiphosphatase and phosphori  
A:Reference number: A45867; MUID:91178501; PMID:1964170  
A:Accession: B45867  
A:Molecule type: DNA  
A:Residues: 1-291 <ME2>  
A:Cross-references: UNIPROT:P23015; EMBL:X17252; NID:g48543; PIDN:CAA35119.1; PID:g48548  
R:Meijer, W.G.; Arnberg, A.C.; Enequist, H.G.; Terpstra, P.; Lidstrom, M.E.; Dijkhuizen,  
Mol. Gen. Genet. 225, 320-330, 1991  
A:Title: Identification and organization of carbon dioxide fixation genes in Xanthobacte  
A:Reference number: S13573; MUID:91172133; PMID:1900916  
A:Accession: S13577  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-291 <ME1>  
A:Cross-references: EMBL:X17252; NID:g48543; PIDN:CAA35119.1; PID:g48548  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989  
C:Genetics:  
A:Gene: cfxP  
C:Superfamily: phosphoribulokinase  
C:Keywords: ATP; Calvin cycle; phosphotransferase

Query Match 72.5%; Score 29; DB 1; Length 291;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0;

QY 1 YVHDA 5  
|||||  
DB 98 YVHDA 102

## RESULT 99

H75512  
formamidopyrimidine-DNA glycosylase - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: H75512  
R:White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: H75512  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-291 <WHI>  
A:Cross-references: GB:AE001908; GB:AE000513; NID:g6458174; PIDN:AAF10070.1; PID:g645817  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR0493  
A:Map position: 1  
C:Superfamily: formamidopyrimidine-DNA glycosidase

Query Match 72.5%; Score 29; DB 2; Length 291;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAP 6  
|||||  
DB 38 VHDAP 42

## RESULT 100

S45461

hypothetical protein YNL006w - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein N2005

C:Species: Saccharomyces cerevisiae  
C>Date: 13-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 16-Aug-2004  
C:Accession: S45461; S62915; S62917; S45123  
R:Verhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.  
Yeast 10, 945-951, 1994

A:Title: Nucleotide sequence analysis of an 8887 bp region of the left arm of yeast chr

A:Reference number: S45461; MUID:95076713; PMID:7985421

A:Accession: S45461

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-303 <VER>

A:Cross-references: UNIPROT:P41318; EMBL:X77114; NID:g496710; PIDN:CAA54380.1; PID:g4567

R:Aert, R.; Verhasselt, P.; Voet, M.; Volckaert, G.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S62910

A:Accession: S62915

A:Molecule type: DNA

A:Residues: 1-303 <AER>

A:Cross-references: EMBL:Z71282; NID:gl301821; PID:e239859; PID:gl301822; MIPS:YNL006w

A:Experimental source: strain S288C

R:Doignon, F.; Crouzet, M.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S62916

A:Accession: S62917

A:Molecule type: DNA

A:Residues: 1-303 <DOI>

A:Cross-references: EMBL:Z71282; NID:gl301821; PID:e239859; PID:gl301822; MIPS:YNL006w

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD.LST8

A:Cross-references: SGD:S0004951

A:Map position: 14L

C:Superfamily: WD repeat homology

F:71-104/Domain: WD repeat homology <WD2>

F:112-145/Domain: WD repeat homology <WD3>

F:203-236/Domain: WD repeat homology <WD5>

F:246-279/Domain: WD repeat homology <WD6>

Query Match 72.5%; Score 29; DB 2; Length 303;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
|:|:|  
DB 113 YKHAPV 119

Search completed: June 30, 2005, 22:23:59  
Job time : 44 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 22:04:54 ; Search time 176 Seconds  
(without alignments)  
20.367 Million cell updates/sec

Title: US-09-874-350C-210

Perfect score: 40

Sequence: 1 YVHDAPV 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	193	2	Q8HXR5
2	40	100.0	269	1	IL1B_HUMAN
3	40	100.0	269	2	Q7RU01
4	39	97.5	651	2	Q9KWR2
5	35	87.5	197	2	Q7MXU9
6	35	87.5	321	1	GLK_ECOLI
7	35	87.5	321	2	Q8FFD4
8	35	87.5	321	2	Q83K86
9	34	85.0	260	2	Q6JFG0
10	34	85.0	303	2	Q7SET3
11	34	85.0	358	2	Q7MCL7
12	33	82.5	206	2	Q62N47
13	33	82.5	268	1	IL1B_MACFA
14	33	82.5	269	1	IL1B_CERTO
15	33	82.5	269	1	IL1B_MACMU
16	33	82.5	269	1	IL1B_MACNE
17	33	82.5	361	1	YHFS_ECOLI
18	33	82.5	361	2	Q7UAS0
19	33	82.5	361	2	Q83JB0
20	33	82.5	361	2	Q8FCW7
21	33	82.5	385	2	Q68CH2
22	33	82.5	406	2	Q714U5
23	33	82.5	414	2	Q7WRG5
24	33	82.5	414	2	Q7WTN2
25	33	82.5	419	1	LPB1_NEIMA
26	33	82.5	419	1	LPB1_NEIMB
27	33	82.5	419	2	Q93JTO
28	33	82.5	422	2	Q7WTM8
29	33	82.5	424	2	Q732T8
30	33	82.5	424	2	Q81A08
31	33	82.5	424	2	Q81WP6

32	33	82.5	424	2	Q6HF27	06hf27 bacillus th
33	33	82.5	581	2	Q7QQ79	Q7qq79 giardia lam
34	33	82.5	586	2	Q8A0E2	Q8a0e2 bacteroides
35	33	82.5	624	2	Q9D2G7	Q9d2g7 mus musculus
36	33	82.5	730	2	Q7RUA4	Q7rua4 neurospora
37	33	82.5	735	1	DNLJ_STRCO	Q9z585 streptomyce
38	33	82.5	740	2	Q6M901	Q6m901 neurospora
39	33	82.5	866	2	Q7ZF80	Q7zf80 cyprinus ca
40	33	82.5	1172	2	Q9VU79	Q9vu79 drosophila
41	33	82.5	1209	2	Q89CK5	Q89ck5 bradyrhizob
42	33	82.5	1249	2	Q812R2	Q812r2 plasmodium
43	33	82.5	1272	2	Q81QK2	Q81qk2 drosophila
44	33	82.5	1286	2	Q7PMF6	Q7pmf6 anopheles g
45	33	82.5	1691	2	Q8AIN9	Q8ayn9 cyprinus ca
46	32	80.0	127	2	Q9ANY4	Q9any4 escherichia
47	32	80.0	203	2	Q43544	Q43544 lilium long
48	32	80.0	206	2	Q94475	Q94475 schizosacch
49	32	80.0	212	1	THIE_STAEP	Q8cnk2 staphylococ
50	32	80.0	220	2	Q72IC3	Q72ic3 thermus the
51	32	80.0	228	1	D7AL_RAT	Q64057 rattus norv
52	32	80.0	260	2	Q6FX28	Q6fx28 candida gla
53	32	80.0	295	1	AMPW_PYRAB	Q9uyt4 pyrococcus
54	32	80.0	295	1	AMPW_PYRHO	Q58362 pyrococcus
55	32	80.0	296	2	Q47402	Q47402 escherichia
56	32	80.0	296	2	Q8GR83	Q8gr83 thermus the
57	32	80.0	306	2	Q8Y917	Q8y917 listeria mo
58	32	80.0	306	2	Q92EB5	Q92eb5 listeria in
59	32	80.0	306	2	Q723A9	Q723a9 listeria mo
60	32	80.0	320	2	Q84CW0	Q84cw0 uncultured
61	32	80.0	343	2	Q9HLG5	Q9hlg5 thermoplasma
62	32	80.0	350	2	Q83VR4	Q83vr4 methylobact
63	32	80.0	353	2	Q9RP68	Q9rp68 pasteurella
64	32	80.0	361	1	CARA_METKA	Q8tyl5 methanopyru
65	32	80.0	372	2	Q830M4	Q830m4 enterococcu
66	32	80.0	382	2	Q65WQ5	Q65wq5 bacillus li
67	32	80.0	387	2	Q9LLZ0	Q9llz0 nymphaea od
68	32	80.0	389	1	XSS5_ECOLI	F42218 escherichia
69	32	80.0	389	2	Q758W7	Q758w7 ashbya goss
70	32	80.0	389	2	Q6KCZ9	Q6kc29 escherichia
71	32	80.0	399	2	Q9NE98	Q9ne98 leishmania
72	32	80.0	405	2	Q9L9K5	Q9l9k5 pasteurella
73	32	80.0	406	2	Q9X5N8	Q9x5n8 escherichia
74	32	80.0	408	2	Q85454	Q85454 pasteurella
75	32	80.0	408	2	Q9CMP3	Q9cmp3 pasteurella
76	32	80.0	412	2	Q8FDP8	Q8fdp8 escherichia
77	32	80.0	445	2	Q6LZW1	Q6lzw1 methanococc
78	32	80.0	454	2	Q8YXA3	Q8yxa3 anabaena sp
79	32	80.0	459	2	Q8SDA3	Q8sda3 galago cras
80	32	80.0	661	2	Q8T2Z0	Q8t2z0 trypanosoma
81	32	80.0	681	2	Q82TW6	Q82tw6 nitrosomona
82	32	80.0	796	2	Q9Q8M8	Q9q8m8 myxoma viru
83	32	80.0	798	2	Q9Q900	Q9q900 rabbit fibr
84	32	80.0	1142	2	Q9P797	Q9p797 schizosacch
85	32	80.0	1345	2	Q8Y282	Q8y282 ralstonia s
86	32	80.0	1871	2	Q9CAG6	Q9cag6 arabidopsis
87	32	80.0	1890	2	Q7G6Z3	Q7g6z3 arabidopsis
88	32	80.0	1894	2	Q64795	Q64795 arabidopsis
89	32	80.0	2110	2	Q8X1E9	Q8x1e9 emericella
90	32	80.0	3044	2	Q7QYR7	Q7qyr7 giardia lam
91	32	80.0	3131	1	VPD2_SCHPO	Q42326 schizosacch
92	32	80.0	5577	2	Q7R1H7	Q7r1h7 giardia lam
93	31	77.5	101	2	Q7N099	Q7n099 photorhabdu
94	31	77.5	103	2	Q6D2T0	Q6d2t0 erwinia car
95	31	77.5	169	2	Q87AH6	Q87ah6 xylella fas
96	31	77.5	169	2	Q9P577	Q9p577 xylella fas
97	31	77.5	205	2	Q6BPB3	Q6bpb3 debaryomyce
98	31	77.5	214	2	Q6IK52	Q6ik52 drosophila
99	31	77.5	228	1	CAPB_STAAB	P39851 staphylococ
100	31	77.5	231	2	Q6U9C3	Q6u9c3 bacteriopho
101	31	77.5	242	2	Q930C8	Q930c3 rhizobium m
102	31	77.5	245	2	Q7XR62	Q7xr62 oryza sativ
103	31	77.5	253	2	Q7SE81	Q7se81 neurospora
104	31	77.5	264	2	Q63L99	Q63l99 burkholderi

105 31 77.5 287 2 Q65J56  
 106 31 77.5 298 2 Q6AFW7  
 107 31 77.5 319 1 MRW LACPL  
 108 31 77.5 319 2 Q7MJV0  
 109 31 77.5 321 2 Q8DAC1  
 110 31 77.5 321 2 Q23259  
 111 31 77.5 321 2 Q6MVC7  
 112 31 77.5 359 1 MRW\_BIFLO  
 113 31 77.5 359 2 Q7XVK7  
 114 31 77.5 388 1 VGS5 ICHV1  
 115 31 77.5 388 2 Q8XQJ0  
 116 31 77.5 398 2 Q8HHP3  
 117 31 77.5 459 2 Q8DSH1  
 118 31 77.5 461 2 Q9HEI4  
 119 31 77.5 471 2 Q6LZ06  
 120 31 77.5 479 2 Q6BT22  
 121 31 77.5 485 1 HUS7 MOUSE  
 122 31 77.5 496 1 YEJ7 ECOLI  
 123 31 77.5 496 2 Q8XD76  
 124 31 77.5 496 2 Q9ABE9  
 125 31 77.5 527 2 Q673E8  
 126 31 77.5 556 2 Q7ADB2  
 127 31 77.5 556 2 Q8FGW4  
 128 31 77.5 557 2 Q63LW0  
 129 31 77.5 560 2 Q9HYA3  
 130 31 77.5 561 2 Q62BI2  
 131 31 77.5 631 2 Q9W271  
 132 31 77.5 634 2 Q8YK57  
 133 31 77.5 648 2 Q8H041  
 134 31 77.5 663 2 Q84ES0  
 135 31 77.5 670 2 Q9TCC2  
 136 31 77.5 688 2 Q8BD17  
 137 31 77.5 691 1 DNLJ MYCBO  
 138 31 77.5 691 1 DNLJ MYCTU  
 139 31 77.5 694 1 DNLJ MYCLE  
 140 31 77.5 730 2 Q82JK7  
 141 31 77.5 737 2 Q63LC7  
 142 31 77.5 787 2 Q7PZ22  
 143 31 77.5 1127 2 Q7PZ22  
 144 31 77.5 1133 2 Q93V59  
 145 31 77.5 1171 2 Q9HNB5  
 146 31 77.5 1173 2 Q6NR54  
 147 31 77.5 1294 1 RRPO WCMVM  
 148 31 77.5 1294 1 RRPO WCMVO  
 149 31 77.5 1302 2 Q6CJM9  
 150 30 75.0 1453 2 Q75PR1  
 026510 methanobact

## ALIGNMENTS

RESULT 1  
 Q8HRS PRELIMINARY; PRT; 193 AA.  
 ID Q8HRS  
 AC Q8HRS  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Interleukin-1 beta (Fragment).  
 GN Name=IL1B;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22344682; PubMed=12356774; DOI=10.1074/jbc.M206636200;  
 RA Smith D.E., Ketchum R.R., Moore H., Anderson Z., Reinshaw B.R.,  
 RA Friend D.J., Sims J.E.;  
 RA "A single amino acid difference between human and monkey interleukin  
 RT (IL)-1beta dictates effective binding to soluble type II IL-1  
 RT receptor.";  
 RL J. Biol. Chem. 277:47619-47625(2002).

CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates  
 CC thymocyte proliferation by inducing IL-2 release, B-cell  
 CC maturation and proliferation, and fibroblast growth factor  
 CC activity (By similarity).  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 DR EMBL: AV172104; AAN76443.1; -.  
 DR HSP; P01584; 211B.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0008283; P:cell proliferation; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0006954; P:inflammatory response; IEA.  
 DR GO; GO:0000074; P:regulation of cell cycle; IEA.  
 DR InterPro; IPR008996; Cytok\_IL1\_like.  
 DR InterPro; IPR002348; IL1\_HBGF.  
 DR InterPro; IPR003502; IL1\_propep.  
 DR InterPro; IPR003294; InterleukinIL1AB.  
 DR InterPro; IPR003296; InterleukinIL1B.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR Pfam; PF02394; IL1\_propep; 1.  
 DR PRINTS; PR00262; IL1HBGF.  
 DR PRINTS; PR00264; INTERLEUKIN1.  
 DR PRINTS; PR01359; INTERLEUKIN1B.  
 DR PRINTS; PR01357; INTERLEUKIN1AB.  
 DR ProDom; PD002336; Interleukin\_1; 1.  
 DR SMART; SM00125; IL1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 KW Inflammatory response; Mitogen; Pyrogen.  
 FT NON\_TER 1  
 SQ SEQUENCE 193 AA; 22233 MW; 8C45E22FC3D7FD37 CRC64;  
 Query Match 100.0%; Score 40; DB 2; Length 193;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YVHDAPV 7  
 DB 37 YVHDAPV 43  
 RESULT 2  
 IL1B HUMAN STANDARD; PRT; 269 AA.  
 ID IL1B HUMAN  
 AC P01584; Q96HES; Q9UCT6;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Interleukin-1 beta precursor (IL-1 beta) (Catabolin).  
 GN Name=IL1B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85088517; PubMed=6083565;  
 RA Auron P.E., Webb A.C., Rosenwasser L.J., Mucci S.F., Rich A.,  
 RA Wolff S.M., Dinarello C.A.;  
 RA "Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:7907-7911(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85240547; PubMed=2989698;  
 RA March C.J., Mosley B., Larsen A., Cerretti D.P., Braedt G., Price V.,  
 RA Gillis S., Henney C.S., Kronheim S.R., Grabstein K., Conlon P.J.,  
 RA Hopp T.E., Cosman D.;  
 RA "Cloning, sequence and expression of two distinct human interleukin-1  
 RT complementary DNAs.";  
 RL Nature 315:641-647(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.



RA MEDLINE=87040762; PubMed=3490654;  
RX Clark B.D., Collins K.L., Gandy M.S., Webb A.C., Auron P.E.;  
RT "Genomic sequence for human prointerleukin 1 beta: possible evolution  
from a reverse transcribed prointerleukin 1 alpha gene.";  
RL Nucleic Acids Res. 14:7897-7914(1986).  
[4]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=87248099; PubMed=2954882; DOI=10.1016/0378-1119(87)90398-2;  
RX Bensi G., Raugeli G., Falla E., Carinci V., Buonamassa D.T., Melli M.;  
RA "Human interleukin-1 beta gene.";  
RL Gene 52:95-101(1987).  
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RN SEQUENCE FROM N.A.  
RX MEDLINE=90249285; PubMed=2635664;  
RX Kotenko S.V., Buleonkov M.T., Veiko V.P., Epishin S.M., Lomakin I.B.,  
RA Emel'yanov A.V., Kozlov A.P., Konusova V.G., Kotov A.Y.,  
RA Kurbatova T.V., Reshetnikov V.L., Simbirtsev A.S., Ketlinskii S.A.,  
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prointerleukin-1 beta.";  
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RN SEQUENCE FROM N.A.  
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RN SEQUENCE FROM N.A.  
RX MEDLINE=87156769; PubMed=3493774;  
RX Nishida T., Nishino N., Takano M., Kawai K., Bando K., Masui Y.,  
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RN SEQUENCE FROM N.A.  
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RA Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;  
RT "SeattlesNP, NHLBI HL66682 program for genomic applications, UW-  
FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
[9]  
RN SEQUENCE FROM N.A.  
RX TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Tothiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahay J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
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and mouse cDNA sequences.";  
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RX MEDLINE=88184226; PubMed=3281727;  
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RT "Effects of hematopoietin-1 and interleukin 1 activities on early  
hematopoietic cells of the bone marrow.";

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RN SEQUENCE OF 114-135.  
RX TISSUE=Skin;  
RX MEDLINE=92013781; PubMed=1919436;  
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beta) to an active IL-1 species by human mast cell chymase.";  
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RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
RX MEDLINE=88211543; PubMed=3259176;  
RA Priestle J.P., Schar H.-P., Grutter M.G.;  
RT "Crystal structure of the cytokine interleukin-1 beta.";  
RL EMBO J. 7:339-343(1988).  
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RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=90099325; PubMed=2602367;  
RA Priestle J.P., Schar H.-P., Grutter M.G.;  
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resolution.";  
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RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=90064532; PubMed=2585509;  
RA Finzel B.C., Clancy L.L., Holland D.R., Muchmore S.W.,  
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resolution.";  
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RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH RECEPTOR.  
RX MEDLINE=97215903; PubMed=9062193;  
RA Vigors G.P., Anderson L.J., Caffes P., Brandhuber B.J.;  
RT "Crystal structure of the type-I interleukin-1 receptor complexed with  
interleukin-1beta.";  
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RN STRUCTURE BY NMR.  
RX MEDLINE=90321925; PubMed=2372550;  
RA Driscoll P.C., Gronenborn A.M., Wingfield P.T., Clore G.M.;  
RT "Determination of the secondary structure and molecular topology of  
interleukin-1 beta by use of two- and three-dimensional heteronuclear  
15N-1H NMR spectroscopy.";  
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[17]  
RN STRUCTURE BY NMR.  
RX MEDLINE=91159409; PubMed=2001363;  
RA Clore G.M., Wingfield P.T., Gronenborn A.M.;  
RT "High-resolution three-dimensional structure of interleukin 1 beta in  
solution by three- and four-dimensional nuclear magnetic resonance  
spectroscopy.";  
RL Biochemistry 30:2315-2323(1991).  
CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates  
thymocyte proliferation by inducing IL-2 release, B-cell  
maturation and proliferation, and fibroblast growth factor  
activity. IL-1 proteins are involved in the inflammatory response,  
being identified as endogenous pyrogens, and are reported to  
stimulate the release of prostaglandin and collagenase from  
synovial cells.  
CC -!- SUBUNIT: Monomer.  
CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic  
segment in the precursor sequence suggests that IL-1 is released  
by damaged cells or is secreted by a mechanism differing from that  
used for other secretory proteins.  
CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the  
amino ends of these proteins serve some as yet undefined function.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----

DR EMBL; M15840; AAA74137.1; -;  
DR EMBL; X02532; CAA26372.1; -;  
DR EMBL; X02770; AAA36106.1; -;  
DR EMBL; X04500; CAA28185.1; -;  
DR EMBL; X56087; CAA39567.1; -;  
DR EMBL; M54933; AAA59136.1; -;  
DR EMBL; M15330; AAA59135.1; -;  
DR EMBL; AV137079; AAM88883.1; -;  
DR EMBL; BC008678; AAO08678.1; -;  
DR PIR; A25542; ICHUIB.  
DR PDB; 1H1B; X-ray; @=117-269.  
DR PDB; 1I1B; X-ray; @=117-269.  
DR PDB; 1IOB; X-ray; @=-.  
DR PDB; 1ITB; X-ray; A=117-269.  
DR PDB; 1L2H; X-ray; A=117-269.  
DR PDB; 2I1B; X-ray; @=117-269.  
DR PDB; 2I1B; X-ray; @=117-269.  
DR PDB; 3I1B; X-ray; @=117-269.  
DR PDB; 4I1B; X-ray; @=117-269.  
DR PDB; 4I1B; X-ray; @=117-269.  
DR PDB; 5I1B; X-ray; @=117-269.  
  
Query Match 100.0%; Score 40; DB 1; Length 269;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YVHDAVP 7  
Db 113 YVHDAVP 119  
  
RESULT 3  
Q7RU01 PRELIMINARY; PRT; 269 AA.  
ID Q7RU01  
AC Q7RU01; (T=EMBLrel. 26, Created)  
DT 01-MAR-2004 (T=EMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (T=EMBLrel. 26, Last annotation update)  
DE Pro-interleukin-1-beta.  
GN Name=IL1B (Il1f2);  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20545212; PubMed=110931146;  
RX DOI=10.1002/1521-4141(200011)30:11<3299>3.0.CO;2-S;  
RA Barton J.L., Herbst R., Bosio D., Higgins L., Nicklin M.J.;  
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1  
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";  
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RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;  
RA Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,  
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RA Haldebrandt F.;  
RT "Molecular cloning of the interleukin-1 gene cluster: construction of  
RT an integrated YAC/PAC contig and a partial transcriptional map in the  
RT region of chromosome 2q13";  
RL Genomics 41:370-378(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94245215; PubMed=8188271;  
RA Nicklin M.J.H., Weith A., Duff G.W.;  
RT "A Physical map of the region encompassing the human interleukin-1-  
RT alpha, interleukin-1-beta and interleukin-1 receptor genes";  
RL Genomics 19:382-384(1994).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;  
RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,  
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RT cluster";  
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RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;  
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RT "IL1HY1: A novel interleukin-1 receptor antagonist gene";  
RL Biochem. Biophys. Res. Commun. 263:702-706(1999).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;  
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,  
RA Sims J.E.;  
RT "Four new members expand the interleukin-1 superfamily";  
RL J. Biol. Chem. 275:1169-1175(2000).  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;  
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,  
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,  
RA Young P.R.;  
RT "Identification and initial characterization of four novel members of  
RT the interleukin-1 family";  
RL J. Biol. Chem. 275:10308-10314(2000).  
RN [8]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;  
RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,  
RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;  
RT "Identification and gene organization of three novel members of the  
RT IL-1 family on human chromosome 2";  
RL Genomics 66:213-216(2000).  
RN [9]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;  
RA Pan G., Rissler P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,  
RA Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.;  
RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-  
RT 1Rrp";  
RL Cytokine 13:1-7(2001).  
RN [10]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;  
RA Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Russel J.,  
RA Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;  
RT "Cloning and characterization of IL-1HY2, a novel interleukin-1 family  
RT member";  
RL J. Biol. Chem. 276:20597-20602(2001).  
RN [11]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21359532; PubMed=11466363;  
RA Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,  
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,  
RA Kastelein R.A.;  
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function  
RT as an antagonist and agonist of NF-kB activation through the orphan  
RT IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446";  
RL J. Immunol. 167:1440-1446(2001).  
RN [12]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3;  
RA Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,  
RA Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G.,  
RA Pan Y., Smith D.E., Young P.R.;  
RT "A new nomenclature for the IL-1-family genes";  
RL Trends Immunol. 22:536-537(2001).

CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates  
 CC thymocyte proliferation by inducing IL-2 release, B-cell  
 CC maturation and proliferation, and fibroblast growth factor  
 CC activity (By similarity).  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- MISCELLANEOUS: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
 CC -!- SIMILARITY: Belongs to the IL-1 family.  
 DR EMBL; BN000002; CAD29872.1; -;  
 DR HSP; P01584; 11TB.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005152; F:interleukin-1 receptor antagonist activity; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0006954; P:inflammatory response; IEA.  
 DR InterPro; IPR008996; Cytok IL1-like.  
 DR InterPro; IPR002348; IL1\_HBGF.  
 DR InterPro; IPR003502; IL1\_propep.  
 DR InterPro; IPR003294; InterleukinIL1AB.  
 DR InterPro; IPR003296; InterleukinIL1B.  
 DR InterPro; IPR003297; InterleukinIL1RA.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR Pfam; PF00340; IL1; 1.  
 DR Pfam; PF02394; IL1\_propep; 1.  
 DR PRINTS; PR00262; IL1HSGF.  
 DR PRINTS; PR00264; INTERLEUKIN1.  
 DR PRINTS; PR01359; INTRLEUKINIB.  
 DR PRINTS; PR01360; INTRLEUKINIX.  
 DR PRINTS; PR01357; INTRLEUKINAB.  
 DR ProDom; PD002536; Interleukin\_1; 1.  
 DR PROSITE; PS00253; INTERLEUKIN\_1; 1.  
 KW Inflammatory response; Mitogen; Pyrogen.  
 FT CHAIN 117 269 interleukin-1-beta.  
 SQ SEQUENCE 269 AA; 30748 MW; 9BF73C673C6FD66 CRC64;

Query Match 100.0%; Score 40; DB 2; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 3.9; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;

QY 1 YVHDAFV 7  
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 Db 113 YVHDAFV 119

RESULT 4  
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 AC Q9KWR2;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Glucoamylase TGA.  
 GN Name=tga;  
 OS Thermoactinomyces vulgaris.  
 OC Bacteria; Firmicutes; Bacillales; Thermoactinomycetaceae;  
 OC Thermoactinomycetes.  
 OX NCBI\_TaxID=2026;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R-47;  
 RX MEDLINE=21432651; PubMed=11549021;  
 RA Uotsu-Tomita R., Tonozuka T., Sakai H., Sakano Y.;  
 RT "Novel glucoamylase-type enzymes from Thermoactinomycetes vulgaris and  
 RT Methanococcus jannaschii whose genes are found in the flanking region  
 RT of the alpha-amylase genes.";  
 RL Appl. Microbiol. Biotechnol. 56:465-473 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R-47;  
 RX MEDLINE=93222535; PubMed=7763540;  
 RA Tonozuka T., Ohtsuka M., Mogi S., Sakai H., Ohta T., Sakano Y.;  
 RT "A neopullulanase-type alpha-amylase gene from Thermoactinomycetes  
 RT vulgaris R-47.";  
 RL Biosci. Biotechnol. Biochem. 57:395-401 (1993).

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R-47;  
 RX MEDLINE=96001349; PubMed=7548164; DOI=10.1016/0167-4838(95)00101-Y;  
 RA Tonozuka T., Mogi S., Shimura Y., Ibuka A., Sakai H., Matsuzawa H.,  
 RA Sakano Y., Ohta T.;  
 RT "Comparison of primary structures and substrate specificities of two  
 RT pullulan-hydrolyzing alpha-amylases, TVA I and TVA II, from  
 RT Thermoactinomycetes vulgaris R-47.";  
 RL Biochim. Biophys. Acta 1252:35-42 (1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R-47;  
 RA Pl Y.;  
 RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB029554; BAA97041.1; -;  
 DR EMBL; AB047926; BAB40639.1; -;  
 DR InterPro; IPR008928; Glyco\_trans\_6hp.  
 DR InterPro; IPR006465; Oligosac\_aml.  
 DR TIGRFAMS; TIGR01577; Oligosac\_aml; 1.  
 SQ SEQUENCE 651 AA; 74227 MW; E09D70FD586C3B71 CRC64;

Query Match 97.5%; Score 39; DB 2; Length 651;  
 Best Local Similarity 85.7%; Pred. No. 16; Indels 0; Gaps 0;  
 Matches 6; Conservative 1; Mismatches 0;

QY 1 YVHDAFV 7  
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 Db 71 YVHDAFV 77

RESULT 5  
 Q7MKU9 PRELIMINARY; PRT; 197 AA.  
 ID Q7MKU9;  
 AC Q7MKU9;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Nicotinate (Nicotinamide) nucleotide adenyltransferase.  
 GN Name=nadD; OrderedLocusNames=PG00058;  
 OS Porphyromonas gingivalis (Bacteroides gingivalis).  
 OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;  
 OC Porphyromonadaceae; Porphyromonas.  
 OX NCBI\_TaxID=837;  
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 RP SEQUENCE FROM N.A.  
 RC STRAIN=W83;  
 RX MEDLINE=22829867; PubMed=12949112;  
 RX DOI=10.1128/JB.185.18.5591-5601.2003;  
 RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,  
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,  
 RA Haft D.H., Kolonay J.P., Nelson W.C., Mason T.M., Tallon L., Gray J.,  
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,  
 RA Dewhirst F.E., Fraser C.M.;  
 RT "Complete genome sequence of the oral pathogenic bacterium  
 RT Porphyromonas gingivalis strain W83.";  
 RL J. Bacteriol. 185:5591-5601 (2003).  
 DR EMBL; AE017172; NAQ65308.1; -;  
 DR TIGR; PG0058;  
 DR GO; GO:0016779; P:nucleotidyltransferase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR GO; GO:0003058; P:biosynthesis; IEA.  
 DR GO; GO:0009435; P:NAD biosynthesis; IEA.  
 DR InterPro; IPR004820; Cytidyltransferase.  
 DR InterPro; IPR004821; Cyt\_trans\_rel.  
 DR InterPro; IPR005248; NAMN\_adtrnsfrase.  
 DR Pfam; PF01467; CTP\_transf\_2; 1.  
 DR TIGRFAMS; TIGR00125; cyt tran rel; 1.  
 DR TIGRFAMS; TIGR00482; NAMN\_adtrnsfrase; 1.  
 KW Complete proteome; Nucleotidyltransferase; Transferase.  
 SQ SEQUENCE 197 AA; 23051 MW; 4457E98C4F431AE4 CRC64;

Query Match 87.5%; Score 35; DB 2; Length 197;

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Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6
Db 148 YVHDAP 153

RESULT 6
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AC P46B80; P78276;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Glucokinase (EC 2.7.1.2) (Glucose kinase).
GN Names:glk; OrderedLocNames=b2388, z3654, ECs3268;
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=K12;
RX MEDLINE=97175560; PubMed=9023215;
RA Meyer D., Schneider-Presenius C., Horlacher R., Peist R., Boose W.W.;
RT "Molecular characterization of glucokinase from Escherichia coli K-12.";
RL J. Bacteriol. 179:1298-1306(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MGL655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli-
RT K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouais K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

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RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: Not highly important in E.coli as glucose is transported
CC into the cell by the pts system already as glucose 6-phosphate.
CC -!- CATALYTIC ACTIVITY: ATP + D-glucose = ADP + D-glucose 6-phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the bacterial glucokinase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U22490; AAG64506.1; -
CC EMBL; U00096; AAC75447.1; -
CC EMBL; D90868; BAA16258.1; -
CC EMBL; D90869; BAA16261.1; -
CC EMBL; AE005470; AAG57514.1; -
CC EMBL; AP002561; BAB36691.1; -
CC PIR; A65013; A65013.
CC PIR; D91037; D91037.
CC PIR; F85881; F85881.
CC EcoBASE; EB2791; -.
CC EcoGene; EG12957; glk.
CC HAMAP; MF_00524; -; 1.
CC InterPro; IPR003836; Glucokinase.
CC Pfam; PF02685; Glucokinase; 1.
CC TIGRfam; TIGR00749; glk; 1.
KW ATP-binding; Complete proteome; Glycolysis; Kinase; Transferase.
FT NP_BIND 8 13 ATP (potential).
FT CONFLICT 108 108 I -> N (in Ref. 1).
FT CONFLICT 188 189 RV -> AC (in Ref. 1).
FT CONFLICT 274 274 A -> G (in Ref. 1).
FT SEQUENCE 321 AA; 34723 MW; 2D6CD956641A3823 CRC64;
SQ
Query Match 87.5%; Score 35; DB 1; Length 321;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 290 YVHDIPV 296

RESULT 7
Q8FFD4 PRELIMINARY; PRT; 321 AA.
ID Q8FFD4;
AC Q8FFD4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glucokinase (EC 2.7.1.2).
GN Name:glk; OrderedLocNames=c2927;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.F., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

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Db          290 YVHDIPV 296
|||||
RESULT 9
Q6JFG0      Q6JFG0      PRELIMINARY;      PRT;      260 AA.
ID AC
AC Q6JFG0;
DT 05-JUL-2004 (TReMBLrel.. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Inhibitor of apoptosis protein.
OC Neodiprion lecontei nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OC NCBI_TaxID=249151;
[1] _
RN SEQUENCE FROM N.A.
RP PubMed=15194779; DOI=10.1128/JVI.78.13.7023-7035.2004;
RX Lauson H.A.M., Lucarotti C.J., Kreil P.J., Feng Q., Retnakaran A.
RA Arif B.M.;
RT "Sequence and Organization of the Neodiprion lecontei
RT Nucleopolyhedrovirus Genome";
RL J. Virol. 78:7023-7035(2004).
DR EMBL; AY349019; AAQ99055.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0006916; P:anti-apoptosis; IEA.
DR InterPro; IPR001370; Prot_inh_I32_IAP.
DR Pfam; PF00653; BIR; 2.
DR SMART; SM00238; BIR; 2.
DR PROSITE; PS01282; BIR_REPEAT_1; 1.
DR PROSITE; PS0143; BIR_REPEAT_2; 2.
SQ SEQUENCE 260 AA; 30841 MW; A9C5EC3DA06E4CB3 CRC64;

Query Match      85.08; Score 34; DB 2; Length 260;
Best Local Similarity 57.1%; Pred. NO. 72;
Matches 4; Conservative 2; Mismatches 1; Indels 0;

QY          1 YVHDAPV 7
|||||
DB          207 YIHDTPI 213

RESULT 10
Q75ET3      Q75ET3      PRELIMINARY;      PRT;      303 AA.
ID AC
AC Q75ET3;
DT 05-JUL-2004 (TReMBLrel.. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE AAL009Cp.
GN ORFNames=AAL009C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OC NCBI_TaxID=33169;
[1] _
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 10895;
RC Dietrich F.S., Voegelé S.E., Brachat S., Lerch A., Gaffney T.,
RA Philippsen P.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 7 WD repeats.
OC EMBL; AE016814; AAS50357.1; -.
DR AGD; AAL009C; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 2.
DR SMART; SM00320; WD40; 6.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_4.
DR PROSITE; PS50082; WD_REPEATS_2; 5.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.

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SQ SEQUENCE 303 AA; 33932 MW; 62C5D3FB19BE3B77 CRC64;
Query Match 85.0%; Score 34; DB 2; Length 303;
Best Local Similarity 85.7%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
| | | | |
DB 113 YKHDAVP 119

RESULT 11
Q7MCL7 PRELIMINARY; PRT; 358 AA.
AC Q7MCL7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein VVA1369.
GN OrderedLocusNames=VVA1369; YJ016).
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AP005350; BAC97395.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 358 AA; 39747 MW; 2F126CB19B169BE0 CRC64;

Query Match 85.0%; Score 34; DB 2; Length 358;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
| | | | |
DB 69 WIHDAVP 75

RESULT 12
Q62N47 PRELIMINARY; PRT; 206 AA.
AC Q62N47;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=BMA0009;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarrisa S.,
RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
DR Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
DR EMBL; CP000010; AAU50074.1; -.
KW Hypothetical protein.
```

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SQ SEQUENCE 206 AA; 21107 MW; 062B7476FD93CCFB CRC64;
Query Match 82.5%; Score 33; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7
| | | | |
DB 59 VHDAPV 64

RESULT 13
IL1B MACFA STANDARD; PRT; 268 AA.
ID IL1B MACFA
AC P79182;
DT 15-JUL-1998 (Rel. 36, Created)
DT 05-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN Name=IL1B;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Thymus;
RA Totsuba K., Takakura H., Hashimoto O., Tatsumi M.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates
CC thymocyte proliferation by inducing IL-2 release. B-cell
CC maturation and proliferation, and fibroblast growth factor
CC activity. IL-1 proteins are involved in the inflammatory response,
CC being identified as endogenous pyrogens, and are reported to
CC stimulate the release of prostaglandin and collagenase from
CC synovial cells (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic
CC segment in the precursor sequence suggests that IL-1 is released
CC by damaged cells or is secreted by a mechanism differing from that
CC used for other secretory proteins.
CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the
CC amino ends of these proteins serve some as yet undefined function.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D63353; BAA09677.1; -.
DR HSSP; P01584; IL2H
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF
DR PRINTS; PR00264; INTERLEUKIN1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Inflammatory response; Macrophage; Mitogen; Pyrogen.
FT PROPEP 1 116 By similarity.
FT CHAIN 117 268 Interleukin-1 beta.
SQ SEQUENCE 268 AA; 30425 MW; CFB7266E3E2C05B4 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 268;
```

Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
| | | | |  
Db 114 VHDAPV 119

## RESULT 14

IL1B CERTO STANDARD; PRT; 269 AA.  
AC P46638;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 03-JUL-2004 (Rel. 44, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta).  
GN Name=IL1B;  
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Cercopithecidae;  
OC NCBI\_TaxID=9531;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=96003435; PubMed=7561102;  
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;  
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";  
RL J. Immunol. 155:3946-3954(1995).  
CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates thymocyte proliferation by inducing IL-2 release, B-cell maturation and proliferation, and fibroblast growth factor activity. IL-1 proteins are involved in the inflammatory response, being identified as endogenous pyrogens, and are reported to stimulate the release of prostaglandin and collagenase from synovial cells.  
CC -!- SUBUNIT: Monomer.  
CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic segment in the precursor sequence suggests that IL-1 is released by damaged cells or is secreted by a mechanism differing from that used for other secretory proteins.  
CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the amino ends of these proteins serve some as yet undefined function.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
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CC EMBL; U19837; AAA86704.1; -;  
CC HSSP; P01584; IL2H.  
CC InterPro; IPR008996; Cytok IL1 like.  
CC InterPro; IPR002348; IL1\_HBGF.  
CC InterPro; IPR003502; IL1\_propep.  
CC InterPro; IPR000975; Interleukin\_1.  
CC Pfam; PF00340; IL1; 1.  
CC Pfam; PF02394; IL1\_propep; 1.  
CC PRINTS; PR00262; IL1HBGF.  
CC PRINTS; PR00264; INTERLEUKIN1.  
CC ProDom; PD002536; Interleukin\_1; 1.  
CC SMART; SM00125; IL1; 1.  
CC PROSITE; PS00253; INTERLEUKIN\_1; 1.  
CC KW Cytokine; Inflammatory response; Macrophage; Mitogen; Pyrogen.  
FT PROPEP 116 By similarity.  
FT CHAIN 117 269 Interleukin-1 beta.  
SQ SEQUENCE 269 AA; 30445 MW; 750AD658D63E83CD CRC64;

Query Match

82.5%; Score 33; DB 1; Length 269;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
| | | | |  
Db 114 VHDAPV 119

## RESULT 15

IL1B MACMU STANDARD; PRT; 269 AA.  
AC P48030;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta).  
GN Name=IL1B;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Cercopithecidae;  
OC NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=96003435; PubMed=7561102;  
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;  
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";  
RL J. Immunol. 155:3946-3954(1995).  
CC -!- FUNCTION: Produced by activated macrophages, IL-1 stimulates thymocyte proliferation by inducing IL-2 release, B-cell maturation and proliferation, and fibroblast growth factor activity. IL-1 proteins are involved in the inflammatory response, being identified as endogenous pyrogens, and are reported to stimulate the release of prostaglandin and collagenase from synovial cells.  
CC -!- SUBUNIT: Monomer.  
CC -!- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic segment in the precursor sequence suggests that IL-1 is released by damaged cells or is secreted by a mechanism differing from that used for other secretory proteins.  
CC -!- DOMAIN: The similarity among the IL-1 precursors suggests that the amino ends of these proteins serve some as yet undefined function.  
CC -!- SIMILARITY: Belongs to the IL-1 family.  
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CC EMBL; U19845; AAA86709.1; -;  
CC HSSP; P01584; IL2H.  
CC InterPro; IPR008996; Cytok IL1 like.  
CC InterPro; IPR002348; IL1\_HBGF.  
CC InterPro; IPR003502; IL1\_propep.  
CC InterPro; IPR000975; Interleukin\_1.  
CC Pfam; PF00340; IL1; 1.  
CC Pfam; PF02394; IL1\_propep; 1.  
CC PRINTS; PR00262; IL1HBGF.  
CC PRINTS; PR00264; INTERLEUKIN1.  
CC ProDom; PD002536; Interleukin\_1; 1.  
CC SMART; SM00125; IL1; 1.  
CC PROSITE; PS00253; INTERLEUKIN\_1; 1.  
CC KW Cytokine; Inflammatory response; Macrophage; Mitogen; Pyrogen.  
FT PROPEP 116 By similarity.  
FT CHAIN 117 269 Interleukin-1 beta.  
SQ SEQUENCE 269 AA; 30481 MW; A7CD59EBAC120BEC7 CRC64;

Query Match

82.5%; Score 33; DB 1; Length 269;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
|||||  
Db 114 VHDAPV 119

RESULT 16  
IL1B\_MACNE STANDARD; PRT; 269 AA.  
AC P51493;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta).  
GN Names=IL1B;  
OS Macaca nemestrina (Pig-tailed macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9545;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=96003435; PubMed=7561102;  
RA Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;  
RT "Comparative sequence analysis of cytokine genes from human and  
nonhuman primates.";  
RL J. Immunol. 155:3946-3954(1995).  
CC -|- FUNCTION: Produced by activated macrophages, IL-1 stimulates  
CC thymocyte proliferation by inducing IL-2 release, B-cell  
CC maturation and proliferation, and fibroblast growth factor  
CC activity. IL-1 proteins are involved in the inflammatory response,  
CC being identified as endogenous pyrogens, and are reported to  
CC stimulate the release of prostaglandin and collagenase from  
CC synovial cells.  
CC -|- SUBUNIT: Monomer.  
CC -|- SUBCELLULAR LOCATION: Secreted. The lack of a specific hydrophobic  
CC segment in the precursor sequence suggests that IL-1 is released  
CC by damaged cells or is secreted by a mechanism differing from that  
CC used for other secretory proteins.  
CC -|- DOMAIN: The similarity among the IL-1 precursors suggests that the  
CC amino ends of these proteins serve some as yet undefined function.  
CC -|- SIMILARITY: Belongs to the IL-1 family.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U19853; AAA86715.1; -;  
CC HSP; P01584; IL2H.  
CC InterPro; IPR008996; Cytok IL1-like.  
CC InterPro; IPR002348; IL1\_HBGF.  
CC InterPro; IPR003502; IL1\_propep.  
CC InterPro; IPR000975; Interleukin\_1.  
CC Pfam; PF00340; IL1\_1.  
CC Pfam; PF02394; IL1\_propep; 1.  
CC PRINTS; PR00262; IL1HBGF.  
CC PRINTS; PR00264; INTERLEUKIN1.  
CC ProDom; PD002536; Interleukin\_1; 1.  
CC SMART; SM00125; IL1; 1.  
CC PROSITE; PS00253; INTERLEUKIN\_1; 1.  
KW Cytokine; Inflammatory response; Macrophage; Mitogen; Pyrogen.  
FT PROPEP 1 By similarity.  
FT CHAIN 116 Interleukin-1 beta.  
FT CHAIN 117 269 Interleukin-1.  
SQ SEQUENCE 269 AA; 30612 MW; 4E7E9E223EAD3B61 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 269;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
|||||  
Db 114 VHDAPV 119

RESULT 17  
YHFS\_ECOLI STANDARD; PRT; 361 AA.  
ID YHFS\_ECOLI  
AC P45545;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE Hypothetical protein Yhfs.  
DE Name=yhfs; OrderedLocNames=b3376;  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
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CC  
CC EMBL; U18997; AAA58173.1; -;  
CC EMBL; U00096; AAC76401.1; -;  
CC PIR; C65132; C65132.  
CC ECHOBASE; EB2750; -;  
CC EcoGene; EG12914; yhfs.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 361 AA; 38599 MW; 53E152242AD1D95E CRC64;  
  
Query Match 82.5%; Score 33; DB 1; Length 361;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
|||||  
Db 95 VHDAPV 100

RESULT 18  
Q7UASO PRELIMINARY; PRT; 361 AA.  
ID Q7UASO  
AC Q7UASO;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein Yhfs.  
DE Name=yhfs; OrderedLocNames=S4368;  
OS Shigella flexneri.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Shigella.  
OX NCBI\_TaxID=623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2457T;



```
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J.; Goldberg M.B.; Burland V.; Venkatesan M.M.; Deng W.;
RA Fournier G.; Mayhew G.F.; Plunkett G. III; Rose D.J.; Darling A.;
RA Mau B.; Perna N.T.; Payne S.M.; Runyen-Janecky L.J.; Zhou S.;
RA Schwartz D.C.; Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RL Infect. Immun. 71:2775-2786 (2003).
DR EMBL; AB016992; AAP19322.1; -
KW Hypothetical protein.
SQ SEQUENCE 361 AA; 226ACD4683B994A9 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHDAPV 7
Db 95 VHDAPV 100

RESULT 19
Q83JB0 PRELIMINARY; PRT; 361 AA.
AC Q83JB0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein yhfS.
GN Name=yhfS; OrderedLocusNames=SF3394;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q.; Yuan Z.; Xu J.; Wang Y.; Shen Y.; Lu W.; Wang J.; Liu H.;
RA Yang J.; Yang F.; Zhang X.; Zhang J.; Yang G.; Wu H.; Qu D.; Dong J.;
RA Sun L.; Xue Y.; Zhao A.; Gao Y.; Zhu J.; Kan B.; Ding K.; Chen S.;
RA Cheng H.; Yao Z.; He B.; Chen R.; Ma D.; Qiang B.; Wen Y.; Hou Y.;
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441 (2002).
DR EMBL; AE015347; AA44856.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 361 AA; 38562 MW; C9ADC4EA5BC38263 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHDAPV 7
Db 95 VHDAPV 100

RESULT 20
Q8FCW7 PRELIMINARY; PRT; 361 AA.
AC Q8FCW7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein yhfS.
GN Name=yhfS; OrderedLocusNames=c4146;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A.; Burland V.; Plunkett G. III; Redford P.; Roesch P.;
RA Raeko D.; Buckles E.L.; Liou S.-R.; Boutin A.; Hackett J.; Stroud D.;
RA Mayhew G.F.; Rose D.J.; Zhou S.; Schwartz D.C.; Perna N.T.;
RA Mobley H.L.T.; Donnenberg M.S.; Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
DR EMBL; AE016768; AA82584.1; -
KW Complete proteome.
SQ SEQUENCE 361 AA; 38644 MW; 07E042FBF192842E CRC64;

Query Match 82.5%; Score 33; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHDAPV 7
Db 95 VHDAPV 100

RESULT 21
Q68CH2 PRELIMINARY; PRT; 385 AA.
AC Q68CH2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative dehydrogenase alpha subunit.
OS Streptomyces carzinostaticus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1897;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15328113;
RX Otsuka M.; Ichinose K.; Fujii I.; Ebizuka Y.;
RT "Cloning, Sequencing, and Functional Analysis of an Iterative Type I
RT Polyketide Synthase Gene Cluster for Biosynthesis of the Antitumor
RT Chlorinated Polyene Neocarzinil in Streptomyces carzinostaticus."
RL Antimicrob. Agents Chemother. 48:3468-3476 (2004).
DR EMBL; AB097904; BAD38879.1; -
DR InterPro; IPR001017; Dehydrogenase_E1.
DR InterPro; IPR002016; Peroxidase.
DR Pfam; PF00676; E1_dh; 1.
DR PROSITE; PS00435; PEROXIDASE_1; UNKNOWN 1.
SQ SEQUENCE 385 AA; 42687 MW; 581141A647782BB8 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 385;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHDAPV 7
Db 202 VHDAPV 207

RESULT 22
Q714U5 PRELIMINARY; PRT; 406 AA.
AC Q714U5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE HcSB.
GN Name=hcSB;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
```

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=700222;
RX  MEDLINE=22999298; PubMed=14638817;
RX  DOI=10.1128/IAI.71.12.7202-7207.2003;
RA  Satola S.W., Schirmer P.L., Farley M.M.;
RT  "Genetic analysis of the capsule locus of Haemophilus influenzae
RL  serotype f.";
RL  Infect. Immun. 71:7202-7207(2003).
DR  EMBL; AF549211; AAQ12663.1; -
DR  GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR  GO; GO:0015774; P:polysaccharide transport; IEA.
DR  InterPro; IPR007833; Capsule_synth.
DR  Pfam; PF05159; Capsule_synth; 1.
SQ  SEQUENCE 406 AA; 47119 MW; 68EDE9198BED5574 CRC64;

Query Match      82.5%; Score 33; DB 2; Length 406;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 YVHDAVP 7
Db  308 YVHVDVPL 314

RESULT 23
Q7WRG5 PRELIMINARY; PRT; 414 AA.
AC  Q7WRG5;
DT  01-OCT-2003 (TrEMBLrel. 25, Created)
DT  01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  HcsB' (HcsB).
GN  Name=hcsB'; Synonyms=hcsB;
OS  Haemophilus influenzae;
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC  Pasteurellaceae; Haemophilus.
OX  NCBI_TaxID=727;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=1007;
RX  MEDLINE=22646111; PubMed=12761153;
RX  DOI=10.1128/IAI.71.6.3639-3644.2003;
RA  Satola S.W., Schirmer P.L., Farley M.M.;
RT  b and nonencapsulated b capsule-negative variants.";
RL  Infect. Immun. 71:3639-3644(2003).
DR  EMBL; AF549213; AAP42186.1; -
DR  EMBL; AF549213; AAP42197.1; -
DR  GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR  GO; GO:0015774; P:polysaccharide transport; IEA.
DR  InterPro; IPR007833; Capsule_synth.
DR  Pfam; PF05159; Capsule_synth; 1.
SQ  SEQUENCE 414 AA; 48068 MW; F84CC99D5607D927 CRC64;

Query Match      82.5%; Score 33; DB 2; Length 414;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 YVHDAVP 7
Db  314 YVHVDVPL 320

RESULT 24
Q7WTN2 PRELIMINARY; PRT; 414 AA.
AC  Q7WTN2;
DT  01-OCT-2003 (TrEMBLrel. 25, Created)
DT  01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  HcsB.
GN  Name=hcsB;
OS  Haemophilus influenzae;
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC  Pasteurellaceae; Haemophilus.
OX  NCBI_TaxID=727;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=22491 / Serogroup A / Serotype 4A;
RX  MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RX  Parthill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA  Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA  Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA  Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA  Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA  Whitehead S., Spratt B.G., Barrell B.G.;
RT  meningitidis 22491.";
RT  "Complete DNA sequence of a serogroup A strain of Neisseria
RL  Nature 404:502-506(2000).
CC  -!- FUNCTION: Involved in the phospholipid modification of the
CC  capsular polysaccharide, a strong requirement for its
CC  translocation to the cell surface.
CC  -!- SUBCELLULAR LOCATION: Inner membrane-associated (cytoplasmic side)
CC  (Probable).
CC  -----
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CC  -----
CC  EMBL; AL162752; CAB83500.1; -.
DR  FIR; G82012; G82012.
DR  InterPro; IPR007833; Capsule_synth.
DR  Pfam; PF05159; Capsule_synth; 1.

OS  Haemophilus influenzae.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC  Pasteurellaceae; Haemophilus.
OX  NCBI_TaxID=727;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CAB834;
RX  MEDLINE=22646111; PubMed=12761153;
RX  DOI=10.1128/IAI.71.6.3639-3644.2003;
RA  Satola S.W., Schirmer P.L., Farley M.M.;
RT  "Complete sequence of the cap locus of Haemophilus influenzae serotype
RT  b and nonencapsulated b capsule-negative variants.";
RL  Infect. Immun. 71:3639-3644(2003).
DR  EMBL; AF549210; AAP42166.1; -
DR  GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR  GO; GO:0015774; P:polysaccharide transport; IEA.
DR  InterPro; IPR007833; Capsule_synth.
DR  Pfam; PF05159; Capsule_synth; 1.
SQ  SEQUENCE 414 AA; 48041 MW; E0A22B838B16C7F6 CRC64;

Query Match      82.5%; Score 33; DB 2; Length 414;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 YVHDAVP 7
Db  314 YVHVDVPL 320

RESULT 25
LPB1 NEIMA STANDARD; PRT; 419 AA.
ID  LPB1 NEIMA
AC  P57038;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Capsule polysaccharide modification protein lipB.
GN  Name=lipB; OrderedLocusNames=NMA0185;
OS  Neisseria meningitidis (serogroup A);
OC  Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC  Neisseriaceae; Neisseria.
OX  NCBI_TaxID=65699;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=22491 / Serogroup A / Serotype 4A;
RX  MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RX  Parthill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA  Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA  Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA  Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA  Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA  Whitehead S., Spratt B.G., Barrell B.G.;
RT  meningitidis 22491.";
RT  "Complete DNA sequence of a serogroup A strain of Neisseria
RL  Nature 404:502-506(2000).
CC  -!- FUNCTION: Involved in the phospholipid modification of the
CC  capsular polysaccharide, a strong requirement for its
CC  translocation to the cell surface.
CC  -!- SUBCELLULAR LOCATION: Inner membrane-associated (cytoplasmic side)
CC  (Probable).
CC  -----
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CC  -----
CC  EMBL; AL162752; CAB83500.1; -.
DR  FIR; G82012; G82012.
DR  InterPro; IPR007833; Capsule_synth.
DR  Pfam; PF05159; Capsule_synth; 1.
```

KW Complete proteome; Inner membrane; Polysaccharide transport;  
 KW Transport.  
 SQ SEQUENCE 419 AA; 48694 MW; 993175CBF3BB025F CRC64;

Query Match 82.5%; Score 33; DB 1; Length 419;  
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 |||||  
 Db 315 YVHDVPL 321

## RESULT 26

LPBI\_NEIMB STANDARD; PRT; 419 AA;  
 AC Q05014;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Capsule polysaccharide modification protein lipB.  
 GN Name=lipB; OrderedLocNames=NMB0083;  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=491;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B1940 / Serogroup B;  
 RX MEDLINE=93316845; PubMed=8326861;  
 RA Frosch M., Mueller A.;  
 RT "Phospholipid substitution of capsular polysaccharides and mechanisms  
 of capsule formation in *Neisseria meningitidis*.";  
 RL Mol. Microbiol. 8:483-493(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MC58 / Serogroup B;  
 RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;  
 RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,  
 RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,  
 RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,  
 RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,  
 RA Dougherty B.A., Mason T.B., Ciecko A., Parksey D.S., Blair E.,  
 RA Clifton H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,  
 RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,  
 RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,  
 RA Venter J.C.;  
 RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain  
 MC58.";  
 RL Science 287:1809-1815(2000).

CC -1- FUNCTION: Involved in the phospholipid modification of the  
 capsular polysaccharide, a strong requirement for its  
 translocation to the cell surface.

CC -1- SUBCELLULAR LOCATION: Inner membrane-associated (cytoplasmic side)  
 (probable).

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CC EMBL; Z13995; -; NOT ANNOTATED\_CDS.  
 DR EMBL; AE002367; AAP40547.1; -;  
 DR PIR; E81240; E81240.  
 DR TIGR; NMB0083; -;

DR InterPro; IPR007833; Capsule synth.  
 DR Pfam; PF05159; Capsule synth; 1.

KW Complete proteome; Inner membrane; Polysaccharide transport;  
 KW Transport.

FT CONFLICT 410 410 K -> N (in Ref. 1).

FT CONFLICT 413 413 N -> D (in Ref. 1).  
 FT CONFLICT 418 419 VI -> TT (in Ref. 1).  
 SQ SEQUENCE 419 AA; 48701 MW; 096A5E05CB5D8283 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 419;  
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 |||||  
 Db 315 YVHDVPL 321

## RESULT 27

Q93JTO PRELIMINARY; PRT; 419 AA.  
 AC Q93JTO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE LipB.  
 GN Name=lipB;  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=93316845; PubMed=8326861;  
 RA Frosch M., Mueller A.;  
 RT "Phospholipid substitution of capsular polysaccharides and mechanisms  
 of capsule formation in *Neisseria meningitidis*.";  
 RL Mol. Microbiol. 8:483-493(1993).  
 DR EMBL; Z13995; CAC59699.1; -;  
 DR PIR; S32880; S32880.  
 DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.  
 DR GO; GO:0015774; P:polysaccharide transport; IEA.  
 DR InterPro; IPR007833; Capsule synth.  
 DR Pfam; PF05159; Capsule synth; 1.  
 SQ SEQUENCE 419 AA; 48678 MW; 189D6F05CB5D8C63 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 419;  
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 |||||  
 Db 315 YVHDVPL 321

## RESULT 28

Q7WTM8 PRELIMINARY; PRT; 422 AA.  
 AC Q7WTM8;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE HcsB.  
 GN Name=hcsB;  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=373;  
 RX MEDLINE=22646111; PubMed=12761153;  
 RX DOI=10.1128/IAI.71.6.3639-3644.2003;  
 RA Satola S.W., Schirmer P.L., Farley M.M.;  
 RT "Complete sequence of the cap locus of *Haemophilus influenzae* serotype  
 b and nonencapsulated b capsule-negative variants.";  
 RL Infect. Immun. 71:3639-3644(2003).  
 DR EMBL; AF549212; AAP42176.1; -;

```
DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR GO; GO:0015774; P:polysaccharide transport; IEA.
DR InterPro; IPR007833; Capsule synth.
DR Pfam; PF05159; Capsule synth; 1.
SQ SEQUENCE 422 AA; 49082 MW; FB64621830C008EA CRC64;

Query Match 82.5%; Score 33; DB 2; Length 422;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 322 YVHDVPE 328
|:|||||

RESULT 29
ID Q732T8 PRELIMINARY; PRT; 424 AA.
AC Q732T8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE3822;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=22523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RA "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RA adaptations and a large plasmid related to Bacillus anthracis px01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AB017276; AAS42727.1; -.
DR TIGR; BCE3822; -.
DR InterPro; IPR001547; Glyco_hydro_5.
DR InterPro; IPR007863; Peptidase_M16_C.
DR Pfam; PF05193; Peptidase_M16_C; 1.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 424 AA; 48837 MW; 39C9A9956A39DA5C CRC64;

Query Match 82.5%; Score 33; DB 2; Length 424;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6
Db 101 YLHDAP 106
|:|||||

RESULT 30
ID Q81A08 PRELIMINARY; PRT; 424 AA.
AC Q81A08;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Zinc protease (SC 3.4.99.-).
GN OrderedLocusNames=BC3787;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=22690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12712630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,

DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.
DR GO; GO:0015774; P:polysaccharide transport; IEA.
DR InterPro; IPR007833; Capsule synth.
DR Pfam; PF05159; Capsule synth; 1.
SQ SEQUENCE 422 AA; 49082 MW; FB64621830C008EA CRC64;

Query Match 82.5%; Score 33; DB 2; Length 424;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6
Db 101 YLHDAP 106
|:|||||

RESULT 31
ID Q81WP6 PRELIMINARY; PRT; 424 AA.
AC Q81WP6; Q6HUJ9; Q6KP26;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BA3923, BAS3637, GBAA3923;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.B., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RA "The genome sequence of Bacillus anthracis Ames and comparison to
RA closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RA "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Sterner;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB017036; AAP27656.1; -.
DR EMBL; AB017334; AAP30309.1; -.
DR EMBL; AB017225; AAP55940.1; -.
DR TIGR; BA3923; -.
DR TIGR; GBAA3923; -.
DR InterPro; IPR001547; Glyco_hydro_5.
```

DR InterPro: IPR007863; Peptidase\_M16\_C.  
DR Pfam: PF05193; Peptidase\_M16\_C; 1.  
DR PROSITE; PS00659; GLYCOSYL\_HYDROL\_F5; UNKNOWN\_1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 424 AA; 48903 MW; 22DB732ABF8198D8 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 424;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
|:|||||  
Db 101 YLHDAP 106

## RESULT 32

Q6HF27 PRELIMINARY; PRT; 424 AA.  
AC Q6HF27;  
DT 05-JUN-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Insulinase, peptidase family M16 (EC 3.4.-.-).  
GN OrderedLocustNames=BN727.3529;  
OS Bacillus thuringiensis (Subsp. konkukian).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=180856;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97-27;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RT "Complete genome sequence of Bacillus thuringiensis 97-27";  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
RE EMBL; AE017355; AA761128.1;  
DR InterPro: IPR001547; Glyco\_hydro.5.  
DR InterPro: IPR007863; Peptidase\_M16\_C.  
DR Pfam: PF05193; Peptidase\_M16\_C; 1.  
DR PROSITE; PS00659; GLYCOSYL\_HYDROL\_F5; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 424 AA; 48921 MW; 22DE623E8A908CD8 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 424;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
|:|||||  
Db 101 YLHDAP 106

## RESULT 33

Q7Q079 PRELIMINARY; PRT; 581 AA.  
AC Q7Q079;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE GLP\_42\_17712.19457.  
OS Giardia lamblia ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.  
OX NCBI\_TaxID=184922;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WB C6;  
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
RA Olsen G.J., Sogin M.L.;  
RT "Draft sequence of the Giardia lamblia genome";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.

DR EMBL; AACB01000153; EAA37169.1; -.  
DR InterPro: IPR001220; Lectin legB.  
DR PROSITE; PS00307; LECTIN LEGUME\_BETA; UNKNOWN\_1.  
SQ SEQUENCE 581 AA; 65294 MW; F40C1EC668DCDC74 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 581;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
|:|||||  
Db 434 YVHDSP 439

## RESULT 34

Q8A0E2 PRELIMINARY; PRT; 586 AA.  
AC Q8A0E2;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
GN OrderedLocustNames=BT4079;  
OS Bacteroides thetaiotaomicron.  
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI\_TaxID=818;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VPI-5482 / ATCC 29148;  
RX MEDLINE=22550838; PubMed=12863928; DOI=10.1126/science.1080029;  
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,  
RA Chiang H.C., Hooper L.V., Gordon J.I.;  
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";  
RL Science 299:2074-2076(2003).  
RE EMBL; AE016943; AA079184.1; -.  
KW Complete proteome.  
SQ SEQUENCE 586 AA; 68999 MW; 7B12CDFE2AD82D9A CRC64;

Query Match 82.5%; Score 33; DB 2; Length 586;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
|:|||||  
Db 177 YLHDAP 182

## RESULT 35

Q9D2G7 PRELIMINARY; PRT; 624 AA.  
AC Q9D2G7;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched  
DE library, clone:4930511N22 product:hypothetical  
DE Esterase/lipase/thioesterase family active site containing protein,  
DE full insert sequence.  
GN Name=Seraci;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Testis;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.

```

RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
  60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
  Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
  Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
  Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
  Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
  sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
  Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
  Hanaoka T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
  Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
  Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
  Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
  Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
  Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
  Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
  Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
  Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RC EMBL; AK019677; BAB31833.1; -
DR MGD; MGI:2447813; Serac1.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR000379; Ser_estr.
KW Hypothetical protein.
SQ SEQUENCE 624 AA; 70677 MW; 6A89D01E57E075E4 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 624;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
DB 76 YVHKAPV 82
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|||||

RESULT 36
Q7RUA4 PRELIMINARY; PRT; 730 AA.
AC Q7RUA4;
DR 01-MAR-2004 (TrEMBLrel. 26, Created)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein B24B19.80.
GN Name=NCU03938.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
  Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
  Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
  Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
  Seitzmunkoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
  Kothke G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
  Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
  Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
  Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
  Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,
  DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
  Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
  Natvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Freitag M.,
  Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
  domain.
CC -!- CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
CC EMBL; AABX01000719; EAA28341.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001138; Fungi_Tfscrp_N.
DR Pfam; PF00172; Zn_clus; 1.
DR PROSITE; PS50048; ZN2_Cy6_FUNGAL_2; 1.
DR DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
  Transcription; Transcription regulation; Zinc.
KW SEQUENCE 730 AA; 78160 MW; 0975281BF403E474 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 730;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6
DB 113 YLHDAP 118
|||||

RESULT 37
DNLJ_STRCO STANDARD; PRT; 735 AA.
AC Q92585;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+]).
GN Name=liga; OrderedLocustNames=SC05494; ORFNames=SC8D9.06;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

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Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S., Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J., Hopwood D.A.,

"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";

Nature 417:141-147(2002).

CC -!- FUNCTION: This protein catalyzes the formation of phosphodiester linkages between 5'-phosphoryl and 3'-hydroxyl groups in double-stranded DNA using NAD as a coenzyme and as the energy source for the reaction. It is essential for DNA replication and repair of damaged DNA (By similarity).

CC -!- CATALYTIC ACTIVITY: NAD(+) + {deoxyribonucleotide}(N) + {deoxyribonucleotide}(M) = AMP + nicotinamide nucleotide + {deoxyribonucleotide}(N+M).

CC -!- SIMILARITY: Belongs to the NAD-dependent DNA ligase family.

CC -!- SIMILARITY: Contains 1 BRCT domain.

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CC -----

DR EMBL; AL399123; CAB37570.1; -.

DR F1R; T35810; T35810.

DR HSP; O87703; 1B04.

DR InterPro; IPR001357; BRCT.

DR InterPro; IPR004150; DNA\_ligase\_OB.

DR InterPro; IPR001679; DNALigase.

DR InterPro; IPR000445; HDH.

DR InterPro; IPR008994; Nucleic\_acid\_OB.

DR InterPro; IPR010994; Ruva\_2\_like.

DR InterPro; IPR004149; Znf\_DNALigase\_C4.

DR Pfam; PF00533; BRCT; 1.

DR Pfam; PF01653; DNA\_ligase\_aden; 1.

DR Pfam; PF03120; DNA\_ligase\_OB; 1.

DR Pfam; PF03119; DNA\_ligase\_ZBD; 1.

DR Pfam; PF003944; DNALigase; 1.

DR SMART; SM00292; BRCT; 1.

DR SMART; SM00532; LIGANC; 1.

DR TIGR; TIGR00575; gnlj; 1.

DR PROSITE; PS01172; BRCT; 1.

DR PROSITE; PS01055; DNA\_LIGASE\_N1; 1.

DR PROSITE; PS01056; DNA\_LIGASE\_N2; FALSE NEG.

DR Complete proteome; DNA repair; DNA replication; Ligase; NAD.

FT DOMAIN 643 713 BRCT.

FT BINDING 130 130 AMP (By similarity).

FT SEQUENCE 735 AA; 80571 MW; 39C4DE1C7CC55930 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 735;  
Best Local Similarity 85.7%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVNDAPV 7  
Db 39 YVNDAPV 45

RESULT 38

ID Q6M901 PRELIMINARY; PRT; 740 AA.

AC Q6M901;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Related to transcriptional regulator RDS2.

GN Name=G17A4.270;

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI\_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA German Neurospora genome project;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster domain.

DR EMBL; BX508812; CA06162.1; -.

DR GO; GO:0005834; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR009079; 4 helix cytokine.

DR InterPro; IPR001138; Fungi\_Tfscrp\_N.

DR Pfam; PF00172; Zn\_c1us; 1.

DR SMART; SM00066; GAL4; 1.

DR PROSITE; PS50048; ZN2\_CY6\_FUNGAL\_2; 1.

DR DNA-binding; Metal-binding; Nuclear protein; Transcription;

DR Transcription regulation; Zinc.

DR SEQUENCE 740 AA; 79511 MW; 17E212530C626A66 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 740;  
Best Local Similarity 83.3%; Pred. No. 3.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
Db 113 YLHDAP 118

RESULT 39

Q7ZT80

ID Q7ZT80 PRELIMINARY; PRT; 866 AA.

AC Q7ZT80;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Truncated isoform of C5-1.

GN Names=C5-1;

OS Cyprinus carpio (Common carp).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;

OC Cyprinidae; Cyprinus.

OX NCBI\_TaxID=7962;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Hepatopancreas;

MDLINE=22505477; PubMed=12618914;

Kato Y., Nakao M., Mutsuro J., Zarkadis I.K., Yano T.;

"The complement component C5 of the common carp (Cyprinus carpio): cDNA cloning of two distinct isotypes that differ in a functional site.";

RL Immunogenetics 54:807-815(2003).

DR EMBL; AB094587; BAC65468.1; -.

DR HSP; P01031; 1KJS.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.

DR InterPro; IPR002890; A2M\_N.

DR InterPro; IPR000020; Anaphylatoxin.

DR InterPro; IPR001599; MacrogloblnA2.

DR Pfam; PF00207; A2M; 1.

DR Pfam; PF01835; A2M\_N; 1.

DR Pfam; PF01821; ANATO; 1.

DR PROSITE: PS01178; ANAPHYLATOXIN 2; 1.  
SQ SEQUENCE 866 AA; 97267 MW; 4EB43F0DASD0CAB8 CRC64;

Query Match 82.5%; -Score 33; DB 2; Length 866;  
Best Local Similarity 85.7%; Pred. NO. 4.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHADPV 7  
||| |||  
Db 254 YVHADPV 260

RESULT 40  
Q9VU79 PRELIMINARY; PRT; 1172 AA.  
AC Q9VU79;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)  
DE CG10738-PA.  
DE ORFNames=CG10738;  
GN Drosophila melanogaster (fruit fly).  
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
[1]  
SEQUENCE FROM N.A.  
RP MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA Sutton G.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA George R.A., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abiril J.P., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Bavendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Borkan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Perrier S., Fleischmann W.,  
RA Foeiler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Morkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheefer F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195 (2000).  
[2]  
SEQUENCE FROM N.A.  
RP MEDLINE=22426065; PubMed=12537569;  
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).  
[3]  
SEQUENCE FROM N.A.  
RP MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).  
[4]  
SEQUENCE FROM N.A.  
RP MEDLINE=22426069; PubMed=12537572;  
RA Mixa S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik K.S.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
systematic review.";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).  
[5]  
SEQUENCE FROM N.A.  
RP FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
[6]  
SEQUENCE FROM N.A.  
RP FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.  
CC -1- SIMILARITY: Belongs to the adenylyl cyclase class-4/guanylyl  
cyclase family.  
CC EMBL; AF003537; AAF49811.1; -.  
DR HSSP; P26769; IAZS.  
DR FlyBase; FBgn0036368; CG10738.  
DR GO; GO:0005524; F-ATP binding; IEA.  
DR GO; GO:0004383; F-guanylate cyclase activity; IEA.  
DR GO; GO:0016829; F-lyase activity; IEA.  
DR GO; GO:0004672; P-protein kinase activity; IEA.  
DR GO; GO:0006182; P:cGMP biosynthesis; IEA.  
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR001828; ANF receptor.  
DR InterPro; IPR01054; G cyclase.  
DR InterPro; IPR01009; Kinase-like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR Pfam; PF01094; ANF receptor; 1.  
DR Pfam; PF00211; Guanylate cyc; 1.  
DR ProDom; PD000001; Prot kinase; 1.  
DR SMART; SM00044; CYCC; 1.  
DR PROSITE; PS00452; GUANYLATE\_CYCLASES\_1; 1.  
DR PROSITE; PS0125; GUANYLATE\_CYCLASES\_2; 1.  
DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.  
KW Lyase; cGMP biosynthesis.  
SQ SEQUENCE 1172 AA; 131992 MW; C6450931P82A6D55 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 1172;  
Best Local Similarity 57.1%; Pred. NO. 5.7e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHADPV 7  
||| |||  
Db 672 YLHDSFI 678

RESULT 41



Q89CK5 Q89CK5 PRELIMINARY; PRT; 1209 AA.  
 AC Q89CK5  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DE BL17792 protein.  
 DE BL17792 protein.  
 GN OrderedLocusNames=bl17792;  
 OS Bradyrhizobium japonicum.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Bradyrhizobium.  
 OX NCBI\_TaxID=375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=USDA110;  
 RX MEDLINE=22484998; PubMed=12597275;  
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
 RA Sasamoto S., Watanabe A., Idesawa K., Iriyuchi M., Kawashima K.,  
 RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,  
 RA Tabata S.;  
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
 RT Bradyrhizobium japonicum USDA110.";  
 RL DNA Res. 9:189-197(2002).  
 DR EMBL; AP005963; BAC53057.1; -  
 DR HSSP; O69771; 1H71.  
 DR GO; GO:000509; F:calcium ion binding; IEA.  
 DR InterPro; IPR01343; Hemlysn\_Ca\_bind.  
 DR InterPro; IPR011050; Pectin\_lyas\_like.  
 DR InterPro; IPR011049; Sertalyan\_like\_C.  
 DR Pfam; PF00353; Hemolysincabind; 4.  
 KW Complete proteome.  
 SQ SEQUENCE 1209 AA; 118292 MW; 50F97581D524EB71 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 1209;  
 Best Local Similarity 83.3%; Pred. No. 5.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
 Db 441 YLHDAP 446

RESULT 42  
 Q812R2 PRELIMINARY; PRT; 1249 AA.  
 AC Q812R2  
 DT 01-WAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein PF11205c.  
 GN Name=PF11205c;  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=36329;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;  
 RA Hall N., Pain A., Berkinin M., Churcher C., Harris B., Harris D.,  
 RA Muncall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,  
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,  
 RA Humphray S., Jagels K., James K.D., Johnson D., Kethornou A.,  
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
 RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,  
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
 RA Sulston J.E., Craig A., Newbold C., Barrell B.G.;  
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";

RL Nature 419:527-531(2002).  
 DR EMBL; AL929357; CAD51927.1; -  
 DR InterPro; IPR000215; Prot inh serpin.  
 DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1249 AA; 147980 MW; 396F6F7CF6199880 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 1249;  
 Best Local Similarity 57.1%; Pred. No. 6.1e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 7  
 Db 927 YIHDIPI 933

RESULT 43  
 Q81QK2 PRELIMINARY; PRT; 1272 AA.  
 AC Q81QK2  
 DT 01-WAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE CG10738-PB.  
 GN ORFNames=CG10738;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;  
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
RA Svirstkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila  
RT melanogaster euchromatic genome sequence.";  
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=22426070; PubMed=12537573;  
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirstkas R.,  
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
RA Ashburner M., Celniker S.E.;  
RT "The transposable elements of the Drosophila melanogaster euchromatin:  
RT a genomics perspective.";  
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
RN [4]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
RT systematic review";  
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
RN [5]  
RN SEQUENCE FROM N.A.  
RP FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RN SEQUENCE FROM N.A.  
RP FlyBase;  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
CC -|- CATALYTIC ACTIVITY: GTP = 3',5'-cyclic GMP + diphosphate.  
CC -|- SIMILARITY: Belongs to the adenylyl cyclase class-4/guanylyl  
CC cyclase family.  
DR EMBL; AE003537; ANL1824.1; -.  
DR HSPSP; P26769; IAZS.  
DR FlyBase; FBgn0036368; CG10738.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004383; F:guanylate cyclase activity; IEA.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0004672; F:protein kinase activity; IEA.  
DR GO; GO:0006182; P:cGMP biosynthesis; IEA.  
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR001828; ANF receptor.  
DR InterPro; IPR001054; G cyclase.  
DR InterPro; IPR011009; Kinase like.  
DR Pfam; PF01094; ANF receptor; 1.  
DR Pfam; PF00211; Guanylate\_cyc; 1.  
DR SMART; SM00044; CYC; 1.  
DR PROSITE; PS00452; GUANYLATE\_CYCLASES\_1; 1.  
DR PROSITE; PS0125; GUANYLATE\_CYCLASES\_2; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW Lyase; cGMP biosynthesis.  
SQ SEQUENCE 1272 AA; 142789 MW; E9BF261470A0D74A CRC64;

Query Match 82.5%; Score 33; DB 2; Length 1272;  
Best Local Similarity 57.1%; Pred. No. 6.3e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
DB 709 YLHDSPI 715

RESULT 44  
Q7PWF6 PRELIMINARY; PRT; 1286 AA.  
AC Q7PWF6; 2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DT ENSANGP00000019379 (Fragment).  
DR Name=ENSANGG00000016890;  
GN Anopheles gambiae str. PEST.  
OS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Anopheles.  
OX NCBI\_TaxID=180454;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PEST;  
RA Anopheles Genome Sequencing Consortium;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -|- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL; AA8901008984; EAA14872.1; -.  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0008270; F:zinc ion binding; IEA.  
DR InterPro; IPR006162; Ppantne S.  
DR InterPro; IPR007087; Znf C2H2.  
DR Pfam; PF00096; Zf-C2H2; 12.  
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN\_1.  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 14.  
DR PROSITE; PS0157; ZINC\_FINGER\_C2H2\_2; 14.  
DR NON\_TER 1286 1286  
SQ SEQUENCE 1286 AA; 141941 MW; FB49E434B7CCB957 CRC64;  
Query Match 82.5%; Score 33; DB 2; Length 1286;  
Best Local Similarity 71.4%; Pred. No. 6.3e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAVP 7  
DB 254 YVHDPVM 260

RESULT 45  
Q8AYN9 PRELIMINARY; PRT; 1691 AA.  
AC Q8AYN9; 2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DT Complement component C5-1.  
DR Name=C5-1;  
OS Cyprinus carpio (Common carp).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxID=7962;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hepatopancreas;  
RC MEDLINE=22505477; PubMed=12618914;  
RA Kato Y., Nakao M., Mutsaers J., Zarkadis I.K., Yano T.;  
RA "The complement component C5 of the common carp (Cyprinus carpio):  
RA cDNA cloning of two distinct isotypes that differ in a functional  
RA site.";  
RT Immunogenetics 54:807-815(2003).  
RL EMBL; AB084635; BAC23057.1; -.  
DR HSSP; P01031; 1KJS.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0004866; F:endorpeptidase inhibitor activity; IEA.  
DR InterPro; IPR002890; AZM\_N.

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DR InterPro; IPR009048; AM_receptor_bind.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001599; Macroglobulin2.
DR InterPro; IPR001134; Netrin C.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01835; A2M_N; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01759; NTR; 1.
DR SMART; SM00643; C345C; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
DR PROSITE; PS01189; NTR; 1.
DR PROSITE; PS01189; NTR; 1.
SQ SEQUENCE 1691 AA; 199778 MW; 488ED2566CC5C8A0 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 1691;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 253 YVHGAPV 259

RESULT 46
Q9ANY4 PRELIMINARY; PRT; 127 AA.
AC Q9ANY4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Capsule export protein KpsB (Fragment).
GN Name=kpsB;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K92;
RX MEDLINE=22590429; PubMed=12578835; DOI=10.1074/jbc.M208837200;
RA Steenbergen S.M., Vimr E.R.;
RT "Functional relationships of the sialyltransferases involved in
RT expression of the polysialic acid capsules of Escherichia coli K1 and
RT K92 and Neisseria meningitidis groups B or C.";
RL J. Biol. Chem. 278:15349-15359(2003).
DR EMBL; AF318310; AAK12093.1; -.
DR GO; GO:0000271; P:polyaccharide biosynthesis; IEA.
DR GO; GO:0015774; P:polyaccharide transport; IEA.
DR InterPro; IPR007833; Capsule_synth.
DR Pfam; PF05159; Capsule_synth; 1.
FT NON_TER 1
SQ SEQUENCE 127 AA; 14793 MW; 6BF512F87A64AAD3 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 127;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db 29 YVHDLPM 35

RESULT 47
Q43544 PRELIMINARY; PRT; 203 AA.
AC Q43544;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Small heat shock protein (Fragment).
GN Name=LjH11;
OS Lilium longiflorum (Trumpet lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC NCBI_TaxID=4690;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Floral bud;
RX MEDLINE=96051386; PubMed=7584025;
RA Kobayashi T., Kobayashi E., Sato S., Hotta Y., Miyazima N., Tanaka A.,
RA Tabata S.;
RT "Characterization of cDNAs induced in meiotic prophase in lily
RT microsporocytes.";
RL DNA Res. 1:15-26(1994).
CC -1- SIMILARITY: Belongs to the small heat shock protein (HSP20)
CC family.
DR EMBL; D21817; BAA04841.1; -.
DR PIR; JC2207; JC2207.
DR HSP; Q41560; IGME.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR002068; Hsp20.
DR InterPro; IPR008978; HSP20_chap.
DR Pfam; PF00011; HSP20; 1.
DR PROSITE; PS01031; HSP20; 1.
KW Heat shock.
FT NON_TER 1
SQ SEQUENCE 203 AA; 21607 MW; A4AFFE5173CB2663 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 203;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6
Db 69 YAHDAAP 74

RESULT 48
O94475 PRELIMINARY; PRT; 206 AA.
AC O94475;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SPCC1919.07 protein.
GN Name=SPCC1919.07;
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weijtens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,
RA Gabel C., Fuchs M., Dusterhoft A., Fritz C., Holzer E., Moestl D.,
RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA Fohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

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RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe."
RA	EMBL; AL035075; CAA22638.1; -
DR	PIR; T41232; T41232
DR	GeneDB SPombe; SPCC1919.07; -
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DR	SEQUENCE 206 AA; 24048 MW; 7A34C9CF2DFCEB60 CRC64;
DR	Query Match 80.0%; Score 32; DB 2; Length 206;
DR	Best Local Similarity 83.3%; Pred. No. 1.5e+02;
DR	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RT  pea.";
RL  Genomics 21:371-378 (1994).
RN  [2]
RP  TISSUE SPECIFICITY.
RX  MEDLINE=98086476; PubMed=9417906; DOI=10.1006/geno.1997.5026;
RA  Skvorak A.B., Robertson N.G., Yin Y., Weremowicz S., Her H.,
RA  Bieber F.R., Beiser K.W., Lynch K.W., Beier D.R., Morton C.C.;
RT  "An ancient conserved gene expressed in the human inner ear:
RT  identification, expression analysis, and chromosomal mapping of human
RT  and mouse antequitin (ATQ1).";
RL  Genomics 46:191-199 (1997).
CC  -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
CC  -1- SUBUNIT: Homotrimer (By similarity).
CC  -1- TISSUE SPECIFICITY: Abundant in kidney, liver, cochlea and outer
CC  hair cells but not inner hair cells or vestibular type I hair
CC  cells. Very low levels in lung, brain, intestine and pancreas.
CC  -1- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
CC  -----
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CC  -----
DR  EMBL; S75019; AAB31967.2; -.
DR  PIR; B54676; B54676.
DR  HSP; P51977; IBSX.
DR  InterPro; IPR02086; Aldehyde_dehydr.
DR  Pfam; PF00111; Aldehyd; 1.
DR  PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; PARTIAL.
DR  PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; PARTIAL.
KW  NAD; Oxidoreductase.
FT  NON_TER 1 19
FT ACT_SITE 19 19 By similarity.
FT SEQUENCE 228 AA; 25157 MW; FSDA69254AF35C16 CRC64;
SQ
Query Match 80.0%; Score 32; DB 1; Length 228;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VHDAPV 7
DB 107 VHDAP 112
-----
RESULT 52
Q6FX28 PRELIMINARY; PRT; 260 AA.
ID Q6FX28
AC Q6FX28;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similarity.
DR ORFNames=CAGL0C007819;
GN Candida glabrata CBS138.
OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jaumaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

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RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR380949; CAG58120.1; -.
SQ SEQUENCE 260 AA; 28711 MW; B6D0050262EBF93 CRC64;
Query Match 80.0%; Score 32; DB 2; Length 260;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YVHDAP 6
DB 109 YVHDAP 114
-----
RESULT 53
AMPN PYRAB STANDARD; PRT; 295 AA.
ID AMPN PYRAB
AC Q5UYT4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Methionine aminopeptidase (EC 3.4.11.18) (MAP) (Peptidase M).
GN Name=map; OrderedLocusNames=PYRAB14230; ORFNames=PAB1434;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
SQ SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RX MEDLINE=22511545; PubMed=12622808;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
RT archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512 (2003).
CC -1- FUNCTION: Removes the amino-terminal methionine from nascent
CC proteins (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
CC preferentially methionine, from peptides and arylamides.
CC -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M24C family.
CC -----
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CC -----
DR EMBL; AJ248287; CAB50328.1; -.
DR PIR; C75054; C75054.
DR HSP; P56218; IXGS.
DR MEROPS; M24.002; -.
DR InterPro; IPR001714; Pept M24 MAP.
DR InterPro; IPR002468; Pept M24A MAP2.
DR InterPro; IPR000994; Peptidase_M24.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00557; Peptidase_M24; 1.
DR PRINTS; PR00599; MAPPEPTIDASE.
DR TIGRFAMs; TIGR00501; met_pdase_II; 1.
DR PROSITE; PS01202; MAP_2; 1.
KW Aminopeptidase; Cobalt; Complete proteome; Hydrolase.
FT METAL 82 82 Cobalt 2 (By similarity).
FT METAL 93 93 Cobalt 1 and 2 (By similarity).

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FT METAL 153 153 Cobalt 1 (By similarity).
FT METAL 187 187 Cobalt 1 (By similarity).
FT METAL 281 281 Cobalt 1 and 2 (By similarity).
SQ SEQUENCE 295 AA; 33027 MW; 2670D3E7DB6BF7B3 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 295;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
|||
Db 208 YVRDAPV 214

RESULT 54
AMPM PYRHO STANDARD; PRT; 295 AA.
AC O58362;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Methionine aminopeptidase (SC 3.4.11.18) (MAP) (Peptidase M).
GN Name-map: OrderedLocusNames=PH0628;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawanabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuwa H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- FUNCTION: Removes the amino-terminal methionine from nascent
CC proteins (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids,
CC preferentially methionine, from peptides and arylamides.
CC -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M24C family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AP000003; BAA29717.1; -.
CC PIR; C71107; C71107.
CC HSPP; P56218; 1XGS.
CC -----
CC MEROPS: M24.002; -.
CC InterPro; IPR001714; Pept_M24_MAP.
CC InterPro; IPR002468; Pept_M24A_MAP2.
CC InterPro; IPR000994; Peptidase_M24.
CC InterPro; IPR009058; Wing_hlx_DNA_bnd.
CC Pfam; PF00557; Peptidase_M24; 1.
CC PRINTS; PR00599; MAPEPTIDASE.
CC TIGRFAMs; TIGR00501; met_pdase_II; 1.
CC PROSITE; PS01202; MAP_2; 1.
CC AminoPeptidase; Cobalt; Complete proteome; Hydrolase.
KW AminoPeptidase; Cobalt; 82
FT METAL 82 82 Cobalt 2 (By similarity).
FT METAL 93 93 Cobalt 1 and 2 (By similarity).
FT METAL 153 153 Cobalt 1 (By similarity).
FT METAL 187 187 Cobalt 1 (By similarity).
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```
FT METAL 280 280 Cobalt 1 and 2 (By similarity).
SQ SEQUENCE 295 AA; 32795 MW; D228F4377CEB2AAC CRC64;

Query Match 80.0%; Score 32; DB 1; Length 295;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
|||
Db 208 YVRDAPV 214

RESULT 55
Q47402 PRELIMINARY; PRT; 296 AA.
ID Q47402;
AC Q47402;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Kps protein (Fragment).
DE Name-Kps;
GN Escherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12/K-1;
RX MEDLINE=92138601; PubMed=1735705;
RA Steenbergen S.M., Wrona T.J., Vimr E.R.;
RT "Functional analysis of the stalyltransferase complexes in Escherichia
RT coli K1 and K92.";
RL J. Bacteriol. 174:1099-1108(1992).
DR EMBL; M76370; AAA24214.1; -.
DR GO; GO:000271; P:polysaccharide biosynthesis; IEA.
DR GO; GO:0015774; P:polysaccharide transport; IEA.
DR InterPro; IPR007833; Capsule_synth.
DR Pfam; PF05159; Capsule_synth; 1.
DR NON_TER 1
FT CHAIN <1 296 Potential.
SQ SEQUENCE 296 AA; 35733 MW; ABEBA3DA46AC308B CRC64;

Query Match 80.0%; Score 32; DB 2; Length 296;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAVP 7
|||
Db 198 YVHDLPM 204

RESULT 56
Q8GR83 PRELIMINARY; PRT; 296 AA.
ID Q8GR83;
AC Q8GR83;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical dehydrogenase protein.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazaki T., Miyazaki J., Nishiyama M., Yamane H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB086412; BAC21188.1; -.
DR GO; GO:0016616; F:oxidoreductase activity, acting on the CH-O...; IEA.
DR GO; GO:0008564; P:ri-berine biosynthesis; IEA.
DR InterPro; IPR006140; 2-Hacid_DH_C.
DR Pfam; PF02826; 2-Hacid_dh_C; 1.
DR PROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
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KW Hypothetical protein.
SQ SEQUENCE 296 AA; 32754 MW; EF48FF11B278E260 CRC64;

Query Match
Best Local Similarity 80.0%; Score 32; DB 2; Length 296;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7
DB 84 IHDAPV 89

RESULT 57
Q81917 PRELIMINARY; PRT; 306 AA.
AC Q81917;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE lmo0541 protein.
GN OrderedLocusNames=lmo0541;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordieik G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591975; CAC98620.1; -.
DR PIR; AF1142; AF1142.
DR ListLib; LMO0541; -.
DR GO; GO:0005381; F:iron ion transporter activity; IEA.
DR GO; GO:0006827; P:high affinity iron ion transport; IEA.
DR Pfam; PF01497; Peripla_BP_2; 1.
DR Complete proteome.
SQ SEQUENCE 306 AA; 33562 MW; 5D3D216C23A5C7D6 CRC64;

Query Match
Best Local Similarity 80.0%; Score 32; DB 2; Length 306;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
DB 198 YVHDAPV 204

RESULT 58
Q92EB5 PRELIMINARY; PRT; 306 AA.
AC Q92EB5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE lmo0545 protein.
GN OrderedLocusNames=lmo0545;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.

Query Match
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
DB 198 YVHDAPV 204

RESULT 59
Q723A9 PRELIMINARY; PRT; 306 AA.
AC Q723A9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ABC transporter, substrate-binding protein.
GN OrderedLocusNames=lmo05365_0570;
OS Listeria monocytogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15115801; DOI=10.1093/nar/gkh562;
RA Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Rasko D.A., Angiuoli S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Nierman W.C., Bean M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Forberger H.A., Tran B., Kathariou S., Wenzel L.D., Uhlir G.A.,
RA Bayles D.O., Luchansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-
borne pathogen Listeria monocytogenes reveal new insights into the
core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL; AE017324; AA03352.1; -.
DR GO; GO:0005381; F:iron ion transporter activity; IEA.
DR GO; GO:0006827; P:high affinity iron ion transport; IEA.
DR InterPro; IPR002491; Peripla_BP.
DR Pfam; PF01497; Peripla_BP_2; 1.
DR Complete proteome.
SQ SEQUENCE 306 AA; 33622 MW; AF082ACC8D3997C6 CRC64;

Query Match
Best Local Similarity 80.0%; Score 32; DB 2; Length 306;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7

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Db 198 YVHDAKV 204
|||||
RESULT 60.
Q84CW0 PRELIMINARY; PRT; 320 AA.
AC Q84CW0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative small subunit ATP sulfurylase.
GN Name=cys6D;
OS uncultured bacterium.
OG Plasmid pAK209.
OC Bacteria; environmental samples.
OX NCBI_TaxID=77133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22560762; PubMed=12673061; DOI=10.1159/000068724;
RA Knietzsch A., Waschkowitz T., Bowien S., Henne A., Daniel R.;
RT "Metagenomes of complex microbial consortia derived from different
RT soils as sources for novel genes conferring formation of carbonyls
RT from short-chain polyols on Escherichia coli.";
RL J. Mol. Microbiol. Biotechnol. 5:46-56(2003).
DR EMBL; AF548448; AA091894.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002500; PAPS reduct.
DR Pfam; PF01507; PAPS_reduct; 1.
KW Plasmid.
SQ SEQUENCE 320 AA; 36581 MW; FF48A90F94747869 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 320;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAKV 7
Db 217 YLHDVPI 223
|||||

RESULT 61
Q9HLG5 PRELIMINARY; PRT; 343 AA.
AC Q9HLG5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Dipeptide transport system permease protein (DPPB) related protein
DE (Putative ABC transporter AbcA1).
GN Name=abcA1; OrderedLocusNames=Ta0263;
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DSM 1728;
RC MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=DSM 1728;
RC Murgunseuk O., Engelhardt H.;
RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
```



OC Pasteurellaceae; Mannheimia.  
 OX NCBI\_TaxID=75985;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21295097; PubMed=11401986;  
 RA DOI=10.1128/IAI.69.7.4458-4464.2001;  
 RA Lo R.Y.C., McKerral L.J., Hills T.L., Kostrzynska M.;  
 RT "Analysis of the capsule biosynthetic locus of Mannheimia  
 (Pasteurella) haemolytica A1 and proposal of a nomenclature system.";  
 RL Infect. Immun. 69:4458-4464 (2001).  
 DR EMBL; AF170495; AAF08251.1; -;  
 DR GO; GO:000271; P:polysaccharide biosynthesis; IEA.  
 DR GO; GO:0015774; P:polysaccharide transport; IEA.  
 DR InterPro; IPR007833; Capsule synth.  
 DR Pfam; PF05159; Capsule\_synth; 1.  
 FT NON TER 353 353  
 SQ SEQUENCE 353 AA; 41854 MW; CBFC2FCCL17F24149 CRC64;  
  
 Query Match 80.0%; Score 32; DB 2; Length 353;  
 Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 1 YVHDAPV 7  
 |::|:  
 Db 306 YIHDVPL 312  
  
 RESULT 64  
 CARA METKA  
 ID \_CARA\_METKA STANDARD; PRT; 361 AA.  
 AC Q8Y15;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain).  
 DE Name=car; OrderedLocNames=MK0491;  
 OS Methanopyrus kandleri.  
 OS Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;  
 OC Methanopyrus.  
 OX NCBI\_TaxID=2320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;  
 RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;  
 RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,  
 RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,  
 RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,  
 RA Malykh A.G., Koonin E.V., Kozayavkin S.A.;  
 RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).  
 CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP + phosphate + L-glutamate + carbamoyl phosphate.  
 CC -1- PATHWAY: Arginine biosynthesis.  
 CC -1- SUBUNIT: Pyrimidine biosynthesis; first step.  
 CC promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).  
 CC -1- SIMILARITY: Belongs to the carA family.  
 CC -1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.  
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 CC EMBL; AA010343; AAM01706.1; -;  
 DR HSSP; P00907; 1CE8.

DR HAMAP; MF\_01209; -; 1.  
 DR InterPro; IPR006274; CarA\_synth\_small.  
 DR InterPro; IPR001317; CP\_synthGATase.  
 DR InterPro; IPR002474; CP\_synthemall.  
 DR InterPro; IPR000991; GATase 1.  
 DR Pfam; PF00988; CPSase\_sm\_chain; 1.  
 DR Pfam; PF00117; GATase\_1\_chain; 1.  
 DR PRINTS; PR00099; CFSGATASE.  
 DR PRINTS; PR00096; GATASE.  
 DR TIGRFAMs; TIGR01368; CFSaseIIsmall; 1.  
 DR PROSITE; PS00442; GATASE TYPE I; 1.  
 KW Arginine biosynthesis; Complete proteome; Glutamine amidotransferase;  
 KW Ligase; Pyrimidine biosynthesis.  
 FT DOMAIN 1 177 CPSase.  
 FT DOMAIN 178 361 Glutamine amidotransferase.  
 FT ACT SITE 252 252 GATase (By similarity).  
 SQ SEQUENCE 361 AA; 39998 MW; ACC6P27ADCC6D6D CRC64;  
  
 Query Match 80.0%; Score 32; DB 1; Length 361;  
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
 Qy 1 YVHDAPV 7  
 |::|:  
 Db 82 YLHDGPI 88  
  
 RESULT 65  
 Q830M4  
 ID Q830M4 PRELIMINARY; PRT; 372 AA.  
 AC Q830M4;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE DNA-damage-inducible protein P.  
 DE Name=dinP; OrderedLocNames=EP2756;  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OS Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=V583 / ATCC 700802;  
 RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;  
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,  
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,  
 RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,  
 RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,  
 RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,  
 RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,  
 RA Fraser C.M.;  
 RT "Role of mobile DNA in the evolution of vancomycin-resistant Enterococcus faecalis";  
 RL Science 299:2071-2074(2003).  
 DR EMBL; AE016955; AA082454.1; -;  
 DR HSSP; P96022; IIM4.  
 DR TIGR; EF2756; -;  
 DR GO; GO:0006281; P:DNA repair; IEA.  
 DR InterPro; IPR001126; UMUC\_like.  
 DR Pfam; PF00817; IMS; 1.  
 DR PROSITE; PS50173; UMUC; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 372 AA; 42368 MW; 9A87041ACCD45869 CRC64;  
  
 Query Match 80.0%; Score 32; DB 2; Length 372;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 YVHDAPV 7  
 |::|:  
 Db 245 IHDAPV 250  
  
 RESULT 66

```

Q65MQ5 Q65MQ5 PRELIMINARY; PRT; 382 AA.
ID Q65MQ5
AC Q65MQ5; (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Cysteine desulfurase).
GN ORFNames=BL00596, BL00723;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 13;
RX PubMed=15383718;
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA Ehrenreich A., Gottschalk G.;
RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an
RT Organism with Great Industrial Potential.";
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; AE017333; AAU39659.1; -
DR EMBL; CP000002; AAU22309.1; -
KW Hypothetical protein.
SQ SEQUENCE 382 AA; 42232 MW; 40F73F0DF4B5496F CRC64;

Query Match 80.0%; Score 32; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7
Db |||||
97 VHDAPV 102

RESULT 67
Q9LLZ0 PRELIMINARY; PRT; 387 AA.
ID Q9LLZ0
AC Q9LLZ0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE NymodLFY protein.
GN Name=NymodLFY;
OS Nymphaea odorata (White water lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; stem Magnoliophyta; Nymphaeales;
OC Nymphaeaceae; Nymphaea.
OX NCBI_TaxID=4419;
RN [1]
RP SEQUENCE FROM N.A.
RA Frohlich M.W., Parker D.S.;
RT "The mostly male theory of flower evolutionary origins: from genes to
RT fossils.";
RL Syst. Bot. 25:158-171(2000).
DR EMBL; AF105110; AAF77609.1; -
DR InterPro; IPR002910; FLO_LFY.
DR Pfam; PF01698; FLO_LFY; 1.
SQ SEQUENCE 387 AA; 42904 MW; 2BA48640DE9E3209 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;

QY 2 VHDAPV 7
Db |||||
97 VHDAPV 102

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 80.0%; Score 32; DB 1; Length 389;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7
Db |||||
303 YVHDAPV 309

RESULT 69
Q758W7 PRELIMINARY; PRT; 389 AA.
ID Q758W7
AC Q758W7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ADR411Wp.
GN ORFNames=ADR411W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Voegel S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,

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RA Philippsen P.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AB016817; AAS52330.1; -  
 DR AGD; ADR411W; -  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003684; F:damaged DNA binding; IEA.  
 DR GO; GO:0004527; F:exonuclease activity; IEA.  
 DR GO; GO:0006281; P:DNA repair; IEA.  
 DR InterPro; IPR003021; Rad1 Rec1.  
 DR PRINTS; PR01245; RAD1REC1.  
 DR SEQUENCE 389 AA; 43153 MW; 2FFFCOA27E7F7CC CRC64;

Query Match 80.0%; Score 32; DB 2; Length 389;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YHDAVP 7  
 Db 225 IHDAPV 230

## RESULT 70

Q6KCZ9 PRELIMINARY; PRT; 389 AA.  
 AC Q6KCZ9;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Capsule polysaccharide export protein KpsS.  
 GN Name=kpsS;  
 GN Escherichia coli.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Nissle 1917;  
 RA Grozdanov L., Raasch C., Schulze J., Sonnenborn U., Gottschalk G.,  
 RA Hacker J., Dobrindt U.;  
 RT "Analysis of the genome structure of probiotic Escherichia coli strain  
 RT Nissle 1917";  
 RL J. Bacteriol. 186:5432-5441 (2004).  
 DR EMBL; AJ586888; CA55819.1; -  
 DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.  
 DR GO; GO:0015774; P:polysaccharide transport; IEA.  
 DR InterPro; IPR007833; Capsule synth.  
 DR Pfam; PF05159; Capsule synth; 1.  
 DR SEQUENCE 389 AA; 46397 MW; FD7AGF73879A2349 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 389;  
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YHDAVP 7  
 Db 303 YHDLPM 309

## RESULT 71

Q9NE98 PRELIMINARY; PRT; 399 AA.  
 AC Q9NE98;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein L4803.06.  
 GN Name=L4803.06;  
 GN Leishmania major.  
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Friedlin;

RX MEDLINE=98146435; PubMed=9477341;  
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
 RA Smith D.F.;  
 RT "A physical map of the Leishmania major Friedlin genome.";  
 RL Genome Res. 8:135-145 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Friedlin;  
 RA Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M.,  
 RA Rajandream M.A., Barrell B.G.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL161416; CAB77684.1; -  
 KW Hypothetical protein.

SQ SEQUENCE 399 AA; 43458 MW; BB86021C2BBB3E18 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 399;  
 Best Local Similarity 66.7%; Pred. No. 3e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YHDAVP 6  
 Db 162 YIHDSF 167

## RESULT 72

Q9L9K5 PRELIMINARY; PRT; 405 AA.  
 AC Q9L9K5;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE LipB.  
 GN LipB.  
 GN Pasteurella multocida.  
 OS Pasteurella multocida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Pasteurella.  
 OX NCBI\_TaxID=747;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M1404;  
 RX MEDLINE=20165152; PubMed=10699509; DOI=10.1016/S0378-1135(99)00193-5;  
 RA Boyce J.D., Chung J.Y., Adler B.;  
 RT "Genetic organisation of the capsule biosynthetic locus of pasteurella  
 RT multocida M1404.";  
 RL Vet. Microbiol. 72:121-134 (2000).  
 DR EMBL; AF169324; AAP67277.1; -  
 DR GO; GO:0000271; P:polysaccharide biosynthesis; IEA.  
 DR GO; GO:0015774; P:polysaccharide transport; IEA.  
 DR InterPro; IPR007833; Capsule synth.  
 DR Pfam; PF05159; Capsule synth; 1.  
 DR SEQUENCE 405 AA; 47636 MW; 1F371B7AA42E7530 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 405;  
 Best Local Similarity 83.3%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YHDAVP 6  
 Db 308 YHDDVP 313

## RESULT 73

Q9X5N8 PRELIMINARY; PRT; 406 AA.  
 AC Q9X5N8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Capsule export protein KpsS.  
 GN Name=kpsS;  
 GN Escherichia coli.  
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.



ID Q6LZM1 PRELIMINARY; PRT; 445 AA.  
AC Q6LZM1;  
DT 05-JUL-2004 (TReMBLrel. 27, Created)  
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
DE Molybdenum containing formylmethanofuran dehydrogenase, subunit B (EC 1.2.99.5).  
DE Name=fmdB; OrderedLocusNames=MMP0512;  
GN Methanococcus maripaludis.  
OS Archaea; Euryarchaeota; Methanococci; Methanococcales;  
OC Methanococcaceae; Methanococcus.  
OX NCBI\_TaxID=39152;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S2 / LL;  
RA Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J., Conway de Macario E., Dodsworth J., Gillett W., Graham D.E., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T., Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G., Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V., Leigh J.A.;  
RA "Complete genome sequence of the mesophilic hydrogenotrophic methanogen Methanococcus maripaludis."  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX957220; CAF30088.1; -;  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR InterPro; IPR006656; Molybdopterin.  
DR Pfam; PF00384; Molybdopterin; 1.  
KW Complete proteome.  
SQ SEQUENCE 445 AA; 49502 MW; B65B6E6CBEE61B69 CRC64;  
Query Match 80.0%; Score 32; DB 2; Length 445;  
Best Local Similarity 71.4%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YVHDAPV 7  
|:|:|:|  
Db 362 YMHDPV 368

RESULT 78  
Q8YXA3 PRELIMINARY; PRT; 454 AA.  
AC Q8YXA3;  
DT 01-MAR-2002 (TReMBLrel. 20, Created)  
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Airl312 protein.  
GN OrderedLocusNames=airl312;  
OS Anabaena sp. (strain PCC 7120).  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
OX NCBI\_TaxID=103690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21595285; PubMed=11759840;  
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;  
RA "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."  
RL DNA Res. 8:205-213(2001).  
DR EMBL; AP003585; BAB73269.1; -;  
DR PIR; AE1970; AE1970.  
DR GO; GO:0003824; F:catalytic activity; IEA.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR Pfam; PF04055; Radical SAM; 1.  
DR Pfam; PF01938; TRAM; 1.  
DR Pfam; PF00919; UPF0004; 1.  
DR SMART; SM00729; Elp3; 1.  
DR TIGRFAMs; TIGR01574; miaB-methiolase; 1.  
DR TIGRFAMs; TIGR00089; UPF0004; 1.

DR PROSITE; PS50926; TRAM; 1.  
DR PROSITE; PS01278; UPF0004; 1.  
KW Complete proteome.  
SQ SEQUENCE 454 AA; 51509 MW; 8606FD00B3D7BDEC CRC64;  
Query Match 80.0%; Score 32; DB 2; Length 454;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YVHDAPV 6  
|:|:|:|  
Db 229 YVHDVP 234

RESULT 79  
Q85DA3 PRELIMINARY; PRT; 459 AA.  
ID Q85DA3;  
AC Q85DA3;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE NADH dehydrogenase subunit 4.  
GN Name=ND4;  
OS Galago crassicaudatus (Thick-tailed galago) (Otolemur crassicaudatus).  
OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.  
OC Mammalia; Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.  
OX NCBI\_TaxID=9463;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521; DOI=10.1073/pnas.1031673100;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RA "A molecular approach to comparative phylogeography of extant Malagasy lemurs."  
RT lemurs."  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
CC -I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
DR EMBL; AF224643; AAP33659.1; -;  
DR GO; GO:0005739; C:mitochondrion; IEA.  
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.  
DR GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.  
DR InterPro; IPR008948; L-Aspartase-like.  
DR InterPro; IPR003918; NADH oxidoreductase.  
DR InterPro; IPR010227; NDH I M.  
DR InterPro; IPR001750; Oxidored q1.  
DR InterPro; IPR000260; Oxidored\_q5\_N.  
DR Pfam; PF00361; Oxidored\_q1; 1.  
DR Pfam; PF01059; Oxidored\_q5\_N; 1.  
DR PRINTS; PR01437; NUOXDRDTASE4.  
DR TIGRFAMs; TIGR01972; NDH I M; 1.  
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.  
SQ SEQUENCE 459 AA; 51525 MW; 9160E2A9E83E187B CRC64;  
Query Match 80.0%; Score 32; DB 2; Length 459;  
Best Local Similarity 57.1%; Pred. No. 3.5e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YVHDAPV 7  
|:|:|:|  
Db 181 YLHDTPI 187

RESULT 80  
Q8T2Z0 PRELIMINARY; PRT; 661 AA.  
ID Q8T2Z0;  
AC Q8T2Z0;  
DT 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Tcc118.1.  
GN Name=Tcc118.1;  
OS Trypanosoma cruzi.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OX NCBI\_TaxID=5693;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CL Brenner;  
 RA Andersson B., Bontempi E.J.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; AC104496; AL96755.1; -;  
 DR HSP; Q93009; INBF.  
 DR GO; GO:0004197; F:Cysteine-type endopeptidase activity; IEA.  
 DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.  
 DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.  
 DR InterPro; IPR000345; CytC heme BS.  
 DR InterPro; IPR001394; Peptidase\_C19.  
 DR Pfam; PF00443; UCH; 1.  
 DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
 DR PROSITE; PS00973; UCH\_2\_2; 1.  
 DR PROSITE; PS0235; UCH\_2\_3; 1.  
 SQ SEQUENCE 661 AA; 73507 MW; FE8CF92C8762E4A6 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 661;  
 Best Local Similarity 85.7%; Pred. No. 5.1e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 |||||  
 Db 339 YVHDADV 345

## RESULT 81

Q82TW6 Q82TW6 PRELIMINARY; PRT; 681 AA.  
 ID Q82TW6  
 AC Q82TW6  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE NAD-dependent DNA ligase (EC 6.5.1.2).  
 GN Nameslig; OrderedLocusNames=NE1753;  
 OS Nitrosomonas europaea.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 OC Nitrosomonadaceae; Nitrosomonas.  
 OX NCBI\_TaxID=915;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19718 / IFO 14298;  
 RX MEDLINE=22586410; PubMed=12700255;  
 RX DOI=10.1128/JB.185.9.2759-2773.2003;  
 RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,  
 RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Savavedra-Soto L.A.,  
 RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;  
 RA "Complete genome sequence of the ammonia-oxidizing bacterium and  
 RT obligate chemolithoautotroph Nitrosomonas europaea";  
 RL J. Bacteriol. 185:2759-2773(2003).  
 CC -1- FUNCTION: This protein catalyzes the formation of phosphodiester  
 CC linkages between 5'-phosphoryl and 3'-hydroxyl groups in double-  
 CC stranded DNA using NAD as a coenzyme and as the energy source for  
 CC the reaction. It is essential for DNA replication and repair of  
 CC damaged DNA (By similarity).  
 CC -1- CATALYTIC ACTIVITY: NAD(+) + {deoxyribonucleotide}(N) +  
 CC {deoxyribonucleotide}(M) = AMP + nicotinamide nucleotide +  
 CC {deoxyribonucleotide}(N+M).  
 CC -1- SIMILARITY: Belongs to the NAD-dependent DNA ligase family.  
 DR ENBL; BX321862; CAD85664.1; -;  
 DR HSP; O87703; I804.  
 DR GO; GO:0005622; C:intracellular; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0003911; F:DNA ligase (NAD+) activity; IEA.  
 DR GO; GO:0016874; F:ligase activity; IEA.  
 DR GO; GO:0006281; P:DNA repair; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR InterPro; IPR001357; BRCT.  
 DR InterPro; IPR001679; DNALigase.  
 DR InterPro; IPR004150; DNA\_ligase\_OB.

DR InterPro; IPR000445; HhH.  
 DR InterPro; IPR003583; HhH\_1.  
 DR InterPro; IPR008994; Nucleic acid\_OB.  
 DR InterPro; IPR010994; Ruva\_2\_like.  
 DR InterPro; IPR004149; Znf\_DNAligase\_C4.  
 DR Pfam; PF00533; BRCT; 1.  
 DR Pfam; PF01653; DNA ligase aden; 1.  
 DR Pfam; PF03120; DNA\_ligase\_OB; 1.  
 DR Pfam; PF03119; DNA\_ligase\_ZBD; 1.  
 DR Pfam; PF00633; HhH; 2.  
 DR ProDom; PD003944; DNALigase; 1.  
 DR SMART; SM00292; BRCT; 1.  
 DR SMART; SM00278; HhH1; 4.  
 DR SMART; SM00532; LIGANC; 1.  
 DR TIGRFAMS; TIGR00575; dnlj; 1.  
 DR PROSITE; PS01172; BRCT; 1.  
 DR PROSITE; PS01056; DNA\_LIGASE\_N2; 1.  
 KW Complete proteome; DNA damage; DNA repair; DNA replication; Ligase;  
 KW NAD.  
 SQ SEQUENCE 681 AA; 75128 MW; 8A25E774E7F34812 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 681;  
 Best Local Similarity 85.7%; Pred. No. 5.3e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAPV 7  
 |||||  
 Db 26 YVQDAPV 32

## RESULT 82

Q908M8 Q908M8 PRELIMINARY; PRT; 796 AA.  
 ID Q908M8  
 AC Q908M8  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE M72L.  
 GN Name=m072L;  
 OS Myxoma virus.  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Leporipoxvirus.  
 OX NCBI\_TaxID=10273;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Lausanne;  
 RX MEDLINE=20032073; PubMed=10562494; DOI=10.1006/viro.1999.0001;  
 RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,  
 RA Macaulay C., Willer D., Evans D., McFadden G.;  
 RA "The complete DNA sequence of myxoma virus";  
 RT Virology 264:298-318(1999).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Lausanne;  
 RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,  
 RA Macaulay C., Willer D., Evans D., McFadden G.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; AF107026; AAF14960.1; -;  
 DR GO; GO:0003700; F:transcription factor activity; IEA.  
 DR InterPro; IPR004974; Pox\_Rap94.  
 DR Pfam; PF03294; Pox\_Rap94; 1.  
 SQ SEQUENCE 796 AA; 93689 MW; 3854D27C10DAD47F CRC64;

Query Match 80.0%; Score 32; DB 2; Length 796;  
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
 |||||  
 Db 771 YVHDVP 776

## RESULT 83

Q9Q900 PRELIMINARY; PRT; 798 AA.

ID Q9Q900 AC Q9Q900

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE GP072L

GN Name=s072L;

OS Rabbit fibroma virus.

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Leporipoxvirus.

OX NCBI\_TaxID=10271;

OX NCBI\_TaxID=10271;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Kasza;

RC MEDLINE=84165064; PubMed=6323741;

RA Delange A.M., Macaulay C., Block W., Mueller T., McFadden G.;

RA "Tumorigenic poxviruses: construction of the composite physical map of

RT the Shope fibroma virus genome.";

RL J. Virol. 50:408-416(1984).

RL [2]

RN SEQUENCE FROM N.A.

RP STRAIN=Kasza;

RC MEDLINE=90266459; PubMed=2161144;

RA Upton C., Ogenorth A., Trakman P., McFadden G.;

RA "Identification and DNA sequence of the Shope fibroma virus DNA

RT topoisomerase gene.";

RL Virology 176:439-447(1990).

RL [3]

RN SEQUENCE FROM N.A.

RP STRAIN=Kasza;

RC MEDLINE=92074222; PubMed=1660196;

RA Strayer D.S., Jering H.H., O'Connor K.;

RA "Sequence and analysis of a portion of the genomes of Shope fibroma

RT virus and malignant rabbit fibroma virus that is important for viral

RT replication in lymphocytes.";

RL Virology 185:585-595(1991).

RL [4]

RN SEQUENCE FROM N.A.

RP STRAIN=Kasza;

RC MEDLINE=20032074; PubMed=10562495; DOI=10.1006/viro.1999.0002;

RA Willer D.O., McFadden G., Evans D.H.;

RA "The complete genome sequence of shope (rabbit) fibroma virus.";

RL Virology 264:319-343(1999).

DR EMBL; AF107222; AAF17954.1; ..

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR InterPro; IPR004974; Pox\_Rap94.

DR Pfam; PF03294; Pox\_Rap94; 1.

SQ SEQUENCE 798 AA; 94394 MW; 788646E84CF20B50 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 798;

Best Local Similarity 83.3%; Pred. No. 6.2e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YHDPAP 6

DB 773 YHDPVP 778

RESULT 84

Q9P797 PRELIMINARY; PRT; 1142 AA.

ID Q9P797 AC Q9P797

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE SPBP35G2.06c protein.

GN Name=SPBP35G2.06c;

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomyces.

OX NCBI\_TaxID=4896;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN=972h-;

RC MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;

RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sources J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth I., Church C.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gatlins S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Walsh S., Warren T., Whitehead S.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schafer M., Muller-Auer S.,

RA Gabel C., Fuchs M., Dusterhoft A., Fritz C., Holzer E., Moestl D.,

RA Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,

RA Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,

RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RT "The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=972h-;

RC Seeger K., Harris D., Wood V., Rajandream M.A., Barrell B.G.;

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL163702; CAB87368.1; ..

DR GeneDB; Srombe; SPBP35G2.06c; ..

DR GO; GO:0005643; C:nuclear pore; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0050658; F:RNA transport; IEA.

DR InterPro; IPR007187; Nup133.

DR Pfam; PF04044; Nup133; 1.

SQ SEQUENCE 1142 AA; 131438 MW; 4A53F86FE19CA82B CRC64;

Query Match 80.0%; Score 32; DB 2; Length 1142;

Best Local Similarity 83.3%; Pred. No. 9.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7

DB 63 IHDAPV 68

RESULT 85

Q8Y282 PRELIMINARY; PRT; 1345 AA.

ID Q8Y282 AC Q8Y282

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE PUTATIVE OXIDOREDUCTASE PROTEIN (EC 1.-.-.-).

GN Name=RS04446; OrderedLocusNames=RSC0454;

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Ralstonia.

OX NCBI\_TaxID=305;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GM11000;

RC MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Ariat M., Billault A., Brottier P., Camus J.C., Catolico L.,

RA Chandler M., Choiane N., Claudel-Renard C., Cunac S., Demange N.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RA Weissenbach J., Boucher C.A.;  
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";  
 RL Nature 415:497-502(2002).

DR EMBL; AL646059; CAD13982.1; --  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR Pfam; PF02754; CCG; 2.  
 DR Pfam; PF02913; FAD-oxidase C; 1.  
 DR Pfam; PF01565; FAD binding\_4; 1.  
 DR PROSITE; PS00198; 4FE4S FERREDOXIN; UNKNOWN\_1.  
 DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN\_1.  
 DR PROSITE; PS00551; MOLYBDOPTERIN\_PROK\_1; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 1345 AA; 149536 MW; 0DE06EA6B917409E CRC64;

Query Match 80.0%; Score 32; DB 2; Length 1345;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
 :|||||  
 Db 348 IHDAPV 353

## RESULT 86

Q9CAG6 PRELIMINARY; PRT; 1871 AA.  
 AC Q9CAG6;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Putative DNA polymerase zeta catalytic subunit.  
 DE Names: F12B7.5;  
 GN Arabidopsis thaliana (Mouse-ear cress).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,  
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,  
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RA Town C.D., Kaul S.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC011020; AGS52299.1; --  
 DR PIR; D96698; D96698.  
 DR GO; GO:0008408; F:3'-5' exonuclease activity; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR InterPro; IPR006172; DNA\_pol\_B.  
 DR InterPro; IPR006134; DNA\_pol\_B\_region.  
 DR Pfam; PF00136; DNA\_pol\_B; 1.  
 DR PRINTS; PR00106; DNAPOLB.  
 DR SMART; SM00486; POLBc; 1.  
 DR PROSITE; PS00116; DNA\_POLYMERASE\_B; 1.  
 DR SEQUENCE 1871 AA; 208639 MW; D3727866B5585EF CRC64;

Query Match 80.0%; Score 32; DB 2; Length 1871;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
 :|||||  
 Db 329 VHDAPV 334

## RESULT 87

Q766Z3 PRELIMINARY; PRT; 1890 AA.  
 AC Q766Z3;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Catalytic subunit of polymerase zeta.  
 DE Name: ACREV3;  
 GN Arabidopsis thaliana (Mouse-ear cress).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=22833953; PubMed=12953110;  
 RA Sakamoto A., Vo L.T., Hase Y., Shikazono N., Matsunaga T., Tanaka A.;  
 RT "Disruption of the ATRV3 gene causes hypersensitivity to ultraviolet  
 RT B light and gamma-rays in Arabidopsis: implication of the presence of  
 RT a translesion synthesis mechanism in plants.";  
 RL Plant Cell 15:2042-2057(2003).  
 DR EMBL; AB114052; BAC82450.1; --  
 DR GO; GO:0008408; F:3'-5' exonuclease activity; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0006260; P:DNA replication; IEA.  
 DR InterPro; IPR006172; DNA\_pol\_B.  
 DR InterPro; IPR006134; DNA\_pol\_B\_region.  
 DR Pfam; PF00136; DNA\_pol\_B; 1.  
 DR PRINTS; PR00106; DNAPOLB.  
 DR SMART; SM00486; POLBc; 1.  
 DR PROSITE; PS00116; DNA\_POLYMERASE\_B; 1.  
 DR SEQUENCE 1890 AA; 210846 MW; 7E3E5BF3C140C105 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 1890;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHDAPV 7  
 :|||||  
 Db 325 VHDAPV 330

## RESULT 88

O64795 PRELIMINARY; PRT; 1894 AA.  
 AC O64795;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Tf15.3 protein.  
 DE Name: Tf15.3;  
 GN Arabidopsis thaliana (Mouse-ear cress).  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Oji, O., Kwan A.,  
 RA Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,  
 RA Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,  
 RA Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,  
 RA Theologis A.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RA Theologis A.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC004393; AAC18785.1; --  
 DR PIR; T02155; T02155.



DR GO: GO:0008408; F:3'-5' exonuclease activity; IEA.  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR GO: GO:0003887; F:DNA-directed DNA polymerase activity; IEA.  
 DR GO: GO:0000166; F:nucleotide binding; IEA.  
 DR GO: GO:0006260; P:DNA replication; IEA.  
 DR InterPro: IPR006172; DNA\_pol\_B.  
 DR InterPro: IPR006134; DNA\_pol\_B\_region.  
 DR Pfam: PF00136; DNA\_pol\_B; 1.  
 DR PRINTS: PR00106; DNAPOB.  
 DR SMART: SM00486; POLBC; 1.  
 DR PROSITE: PS00116; DNA\_POLYMERASE\_B; 1.  
 SQ SEQUENCE 1894 AA; 211356 MW; AE36498D70EFCBF8 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 1894;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VHDAPV 7  
 |::|||  
 Db 329 VHDAPV 334

RESULT 89  
 Q8X1E9 PRELIMINARY; PRT; 2110 AA.  
 AC Q8X1E9  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Calcium channel.  
 GN Namescchi;  
 OS Emericella nidulans (Aspergillus nidulans).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
 OC Eurotiales; Trichocomaceae; Emericella.  
 OX NCBI\_TaxID=162425;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Fischer M., Jackson C., Sanders D.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits family.

DR EMBL: AF393474; AAL37946.1; -.  
 DR GO: GO:001021; C:integral to membrane; IEA.  
 DR GO: GO:0005891; C:voltage-gated calcium channel complex; IEA.  
 DR GO: GO:0005509; F:calcium ion binding; IEA.  
 DR GO: GO:0005245; F:voltage-gated calcium channel activity; IEA.  
 DR GO: GO:0006816; P:calcium ion transport; IEA.  
 DR GO: GO:0006812; P:cation transport; IEA.  
 DR Pfam: PF00520; Ion\_trans; 4.  
 DR PRINTS: PR00167; CCHANNEL.  
 DR Calcium; Calcium channel; Calcium transport; Calcium-binding;  
 KW ion transport; Ionic channel; Transmembrane; Transport;  
 KW Voltage-gated channel  
 SQ SEQUENCE 2110 AA; 237722 MW; B67C66BEA81BF2A4 CRC64;

Query Match 80.0%; Score 32; DB 2; Length 2110;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+03;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
 |::|||  
 Db 284 YVHDAP 289

RESULT 90  
 Q7QYR7 PRELIMINARY; PRT; 3044 AA.  
 AC Q7QYR7  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE GLP\_70\_49040\_39906.

OS Giardia lamblia ATCC 50803.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
 OX NCBI\_TaxID=184922;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WB C6;  
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 RA Olsen G.J., Sogin M.L.;  
 RT "Draft sequence of the Giardia lamblia genome."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL: AACB01000048; EAA40229.1; -.  
 SQ SEQUENCE 3044 AA; 347081 MW; 24F737600F128C6D CRC64;

Query Match 80.0%; Score 32; DB 2; Length 3044;  
 Best Local Similarity 57.1%; Pred. No. 2.6e+03;  
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAPV 7  
 |::|||  
 Db 944 YVHDAPV 950

RESULT 91  
 VPD2 SCHPO STANDARD; PRT; 3131 AA.  
 AC O42976; P78943;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Putative vacuolar protein sorting-associated protein vps1302.  
 GN Names-vps1302; Synonyms-vps13b; ORFNames=SPBC16C6.02c;  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;  
 RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Ruckie E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Pritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey P., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foraburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe."  
 RL Nature 415:871-880(2002).  
 [2]

RP SEQUENCE OF 2999-3131 FROM N.A.  
 RC STRAIN=PR745;  
 RX MEDLINE=98162722; PubMed=9501991;  
 [2]

```
RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RL CDNAS."; 4:363-369(1997).
CC -|- SIMILARITY: Belongs to the VPS13 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AL021767; CAA16910.1; -.
DR EMBL; D89192; BAA13854.1; -.
DR FIR; T39553; T39553.
DR GeneDB SPombe; SPBC16C6.02C; -.
DR InterPro; IPR009543; DUF1162.
DR Pfam; PF06650; DUF1162; 1.
KW Hypothetical protein.
FT CONFLICT 3002 3002 T -> P (in Ref. 2).
FT CONFLICT 3076 3076 H -> T (in Ref. 2).
FT CONFLICT 3115 3115 K -> E (in Ref. 2).
SQ SEQUENCE 3131 AA; 354020 MW; BBD22BE7F668EEF4 CRC64;
Query Match 80.0%; Score 32; DB 1; Length 3131;
Best Local Similarity 83.3%; Pred. No. 2.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 VHDAPV 7
DB 2650 IHDAPV 2655

RESULT 92
Q7RIH7 PRELIMINARY; PRT; 5577 AA.
ID Q7RIH7
AC Q7RIH7
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GLP 38 45618 28885.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RA "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -|- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000027; EAA41168.1; -.
DR GO; GO:0030286; C:dynain complex; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro; IPR000169; Dynein_heavy.
DR InterPro; IPR000169; Pept_cys_acsite.
DR Pfam; PF03028; Dynein_heavy; 1.
DR PROSITE; PS00639; TH10L_PROTEASE_HIS; UNKNOWN 1.
SQ SEQUENCE 5577 AA; 629976 MW; 7DD20BF55E301809 CRC64;
Query Match 80.0%; Score 32; DB 2; Length 5577;
Best Local Similarity 83.3%; Pred. No. 4.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YVHDAP 6
DB 4848 YVHDP 4853
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RESULT 93
Q7N099 PRELIMINARY; PRT; 101 AA.
ID Q7N099
AC Q7N099
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to putative membrane protein YqJD of Escherichia coli.
GN OrderedLocNames=plu3994;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=TT01;
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taurit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Siguer P., Vincent R., Wingate V.,
RA Zouline M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens.";
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571872; CAE16366.1; -.
DR PhotoList; plu3994; -.
DR InterPro; IPR010279; DUF883.
DR Pfam; PF05957; DUF883; 1.
KW Complete proteome.
SQ SEQUENCE 101 AA; 11049 MW; 9728F9B9F3279F5A CRC64;
Query Match 77.5%; Score 31; DB 2; Length 101;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YVHDAP 6
DB 75 YVHDP 80

RESULT 94
Q6D2T0 PRELIMINARY; PRT; 103 AA.
ID Q6D2T0
AC Q6D2T0
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=ECA3015;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauber H., Jagels K., Moule S., Norbertzak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG75914.1; -.
DR InterPro; IPR010279; DUF883.
DR Pfam; PF05957; DUF883; 1.
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KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 103 AA; 11353 MW; 11F8030774C72407 CRC64;

Query Match 77.5%; Score 31; DB 2; Length 103;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
Db 77 YVHDAP 82

RESULT 95  
ID Q87AH6 PRELIMINARY; PRT; 169 AA.  
AC Q87AH6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Transcriptional regulator Fur family.  
GN Name=sur; OrderedLocNames=PD1849;  
OS Xylella fastidiosa (strain Temecual / ATCC 700964).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xylella.  
OX NCBI\_TaxID=183190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22421331; PubMed=12533478;  
RX DOI=10.1128/JB.185.3.1018-1026.2003;  
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,  
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., Ferro M.I.T., da Silva F.R.,  
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,  
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Teai S.M.,  
RA Carrier H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,  
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,  
RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,  
RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,  
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,  
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,  
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,  
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,  
RA Kitajima J.P.;  
RT "Comparative analyses of the complete genome sequences of Pierce's  
RT disease and citrus variegated chlorosis strains of Xylella  
RT fastidiosa";  
RL J. Bacteriol. 185:1018-1026(2003).  
DR ENBL: AE012560; AA029681.1; -;  
DR GO: GO:0003700; P:transcription factor activity; IEA.  
DR GO: GO:006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR00345; CytC\_heme\_BS.  
DR InterPro: IPR002481; FUR.  
DR InterPro: IPR009058; Wing\_hlx\_DNA\_bnd.  
DR Pfam: PF01475; FUR; 1.  
DR ProDom: PD002003; FUR; 1.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 169 AA; 18596 MW; 327704FF9B043007 CRC64;

Query Match 77.5%; Score 31; DB 2; Length 169;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
Db 13 HVHDAP 18

RESULT 96  
ID Q9PF57 PRELIMINARY; PRT; 169 AA.  
AC Q9PF57;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Transcriptional regulator (Fur family).  
GN OrderedLocNames=Xf0821;  
OS Xylella fastidiosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xylella.  
OX NCBI\_TaxID=2371;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=9a5C;  
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;  
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Apiciano M.,  
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,  
RA Coutinho L.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
RA Fraga J.S., Franca S.C., Franco M.C., Frohne M., Furlan L.R.,  
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,  
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
RA de Souza A.P., Terenzi M.F., Truffi D., Teai S.M., Tsuchioka M.H.,  
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;  
RT "The genome sequence of the plant pathogen Xylella fastidiosa";  
RL Nature 406:151-159(2000).  
DR ENBL: AE003922; AAP83631.1; -;  
DR PIR: B82757; B82757.  
DR GO: GO:0003700; P:transcription factor activity; IEA.  
DR GO: GO:006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro: IPR00345; CytC\_heme\_BS.  
DR InterPro: IPR002481; FUR.  
DR InterPro: IPR009058; Wing\_hlx\_DNA\_bnd.  
DR Pfam: PF01475; FUR; 1.  
DR ProDom: PD002003; FUR; 1.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
KW Complete proteome.  
SQ SEQUENCE 169 AA; 18615 MW; 1E19513695B5CF34 CRC64;

Query Match 77.5%; Score 31; DB 2; Length 169;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVHDAP 6  
Db 13 HVHDAP 18

RESULT 97  
ID Q6BPB3 PRELIMINARY; PRT; 205 AA.  
AC Q6BPB3;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to CA4835|IPF1218 Candida albicans IPF1218 Similar to  
DE superoxide dismutase.  
DE ORFNames=DEHA0E15565g;  
GN Debaryomyces Hansenii CBS767.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.  
OX NCBI\_TaxID=284592;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CBS767;  
RG Genolevures;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E., V.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boissame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolaki M., Ozcas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts";  
RL Nature 430:35-44 (2004).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=CBS767;  
RC Genoscope;  
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Destroys radicals which are normally produced within the  
CC cells and which are toxic to biological systems (By similarity).  
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).  
CC -1- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By  
CC similarity).  
CC -1- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.  
DR EMBL; CR382137; CAG88203.1; -.  
DR GO; GO:0004785; F:copper, zinc superoxide dismutase activity; IEA.  
DR GO; GO:0046872; F:metal ion binding; IEA.  
DR GO; GO:0006801; P:superoxide metabolism; IEA.  
DR InterPro; IPR001424; SOD\_CU\_ZN.  
DR Pfam; PF00080; SOD\_Cu; 1.  
DR Copper; Metal-binding; Oxidoreductase; Zinc.  
SQ SEQUENCE 205 AA; 21058 MW; 54EAE38D165B3D20 CRC64;  
  
Query Match 77.5%; Score 31; DB 2; Length 205;  
Best Local Similarity 71.4%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YVHDAPV 7  
:|:|:|  
Db 75 HVHEAPV 81  
  
RESULT 98  
Q6IK52 PRELIMINARY; PRT; 214 AA.  
AC Q6IK52;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE HDC13360.  
GN ORFNames=HDC13360;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14709175; DOI=10.1186/gb-2003-5-1-r3;  
RA Hild M., Beckmann B., Haas S., Koch B., Solovyev V., Busold C.,  
RA Fellenberg K., Boutsou M., Vingron M., Sauer F., Hohnsbeil J., Paro R.;  
RA "An integrated gene annotation and transcriptional profiling approach  
RT towards the full gene content of the Drosophila genome.";  
RL Genome Biol. 5:R3-R3(2003).  
  
CC -1- MISCELLANEOUS: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.  
DR EMBL; BK02514; DAA04020.1; - 273FC26975CDDL1C1 CRC64;  
SQ SEQUENCE 214 AA; 23883 MW; 273FC26975CDDL1C1 CRC64;  
  
Query Match 77.5%; Score 31; DB 2; Length 214;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YVHDAP 6  
:|:|:|  
Db 132 YIHDCP 137  
  
RESULT 99  
CAPB\_STAAU STANDARD; PRT; 228 AA.  
ID CAPB\_STAAU STANDARD; PRT; 228 AA.  
AC P39851;  
DT 01-PEB-1995 (Rel. 31, Created)  
DT 01-PEB-1995 (Rel. 31, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Putative tyrosine-protein kinase capB (EC 2.7.1.112).  
GN Name=capB;  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N;  
RX MEDLINE=95050273; PubMed=7961465;  
RA Lin W.S., Gunneen T., Lee C.Y.;  
RT "Sequence analysis and molecular characterization of genes required  
RT for the biosynthesis of type 1 capsular polysaccharide in  
RT Staphylococcus aureus.";  
RL J. Bacteriol. 176:7005-7016(1994).  
CC -1- FUNCTION: Required for the biosynthesis of type 1 capsular  
CC polysaccharide.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- PATHWAY: Capsular polysaccharide (CPS) biosynthesis.  
CC -1- SIMILARITY: Belongs to the cpsD/capB family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U10927; AAA64641.1; -.  
DR InterPro; IPR005702; EPS\_synthesis.  
DR TIGRFAMs; TIGR01007; eps\_fam; 1.  
KW Bacterial capsule; Exopolysaccharide synthesis; Transferase;  
KW Tyrosine-protein kinase.  
SQ SEQUENCE 228 AA; 25176 MW; 777A4395AA8D7F67 CRC64;  
  
Query Match 77.5%; Score 31; DB 1; Length 228;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YVHDAP 6  
:|:|:|  
Db 12 YVHDKP 17  
  
RESULT 100  
Q6U9R8 PRELIMINARY; PRT; 231 AA.  
ID Q6U9R8  
AC Q6U9R8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE DCMP hydroxymethylase.  
OS Bacteriophage 4RR2.8c.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
OC T4-like viruses.  
OX NCBI\_TaxID=115987;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nolan J.M., Petrov V., Bertrand C., Krisch H.M., Karam J.D.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY375531; AA081353.1; -  
DR HSP; P08773; 1B5E.  
DR GO: 0008168; F:methyltransferase activity; IEA.  
DR GO: 0004799; F:thymidylate synthase activity; IEA.  
DR GO: 0006231; P:dTMP biosynthesis; IEA.  
DR InterPro; IPR000398; Thymidylat\_synth.  
DR ProDom; PD001180; Thymidylat\_synth; 2.  
KW Methyltransferase.  
SQ SEQUENCE 231 AA; 26856 MW; B6EB63F272CCE43E CRC64;

Query Match 77.5%; Score 31; DB 2; Length 231;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YVHDAP 6  
| | | | |  
Db 68 YVHDIP 73

Search completed: June 30, 2005, 22:22:47  
Job time : 185 secs

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